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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2005, 05:43:39 ; Search time 201 Seconds
(without alignments)
2165.421 Million cell updates/sec

Title: US-09-778-963B-2

Perfect score: 1377
Sequence: 1 MKMTLSGNCCTLSVPANNSY.....IKAVLRGQAREKDKCTIQ 266

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Ygapop 10.0 , Ygapext 0.5
Rgapop 6.0 , Rgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QMT=fastap -SUFFIX=rml -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsu62 -TRANS=human40.cdt
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-RGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1372	99.6	837	4	US-09-709-103-40
2	1372	99.6	837	4	US-09-439-410A-40
3	1372	99.6	837	4	US-09-949-016-5022
4	911	66.2	9259	4	US-09-949-016-16764
5	879	63.8	846	4	US-09-709-103-11
6	879	63.8	846	4	US-09-439-410A-1
7	879	63.8	1740	4	US-09-709-103-45
8	879	63.8	1740	4	US-09-439-410A-45
9	879	63.8	1801	4	US-09-709-103-3
10	879	63.8	1801	4	US-09-439-410A-3
11	879	63.8	1841	3	US-09-053-374A-1
12	876.5	63.7	1689	3	US-09-053-374A-4

13	820	59.5	3079	3	US-09-053-374A-6	Sequence 6, Appl
14	817	59.3	3986	3	US-09-053-374A-3	Sequence 3, Appl
15	817	59.3	4990	4	US-09-439-410A-73	Sequence 73, Appl
16	344	25.0	1108	4	US-09-620-512D-945	Sequence 945, Appl
17	298	21.6	432	4	US-09-621-976-17745	Sequence 17745, A
18	294.5	21.4	3300	4	US-09-620-312D-456	Sequence 456, Appl
19	285	20.7	615	1	US-08-247-946A-5	Sequence 5, Appl
20	285	20.7	615	1	PCT-US95-06420-5	Sequence 5, Appl
21	280.5	20.4	551	4	US-09-765-298A-25	Sequence 25, Appl
22	280.5	20.4	567	4	US-09-223-88-1	Sequence 1, Appl
23	280.5	20.4	570	3	US-08-884-866A-2	Sequence 2, Appl
24	280.5	20.4	4480	3	US-09-167-122-12	Sequence 12, Appl
25	279.5	20.3	570	3	US-08-884-866A-11	Sequence 11, Appl
26	279.5	20.3	5775	1	US-08-106-621B-15	Sequence 15, Appl
27	279.5	20.3	5775	1	US-09-023-655-1145	Sequence 1145, Ap
28	279.5	20.3	5775	4	US-09-949-016-702	Sequence 702, Appl
29	279.5	20.3	5775	5	PCT-US93-06251-29	Sequence 29, Appl
30	278.5	20.2	567	4	US-09-223-588-2	Sequence 2, Appl
31	278.5	20.2	1368	4	US-09-949-016-4767	Sequence 4767, Ap
32	277.5	20.2	480	3	US-08-884-866A-9	Sequence 9, Appl
33	277.5	20.2	570	4	US-09-765-298A-27	Sequence 27, Appl
34	277.5	20.2	607	2	US-08-429-964-85	Sequence 85, Appl
35	274.5	19.9	711	4	US-09-248-796A-5513	Sequence 5513, Ap
36	274	19.9	2436	1	US-08-306-691B-16	Sequence 16, Appl
37	274	19.9	2436	4	US-09-963-137-161	Sequence 161, Appl
38	274	19.9	2436	4	US-09-963-137-165	Sequence 165, Appl
39	273.5	19.9	574	2	US-08-429-964-83	Sequence 83, Appl
40	269.5	19.6	798	4	US-09-248-796A-5510	Sequence 5510, Ap
41	269.5	19.6	3026	4	US-09-963-137-136	Sequence 136, Appl
42	269.5	19.6	3026	4	US-09-963-137-140	Sequence 140, Appl
43	255.5	18.6	450	3	US-08-884-866A-10	Sequence 10, Appl
44	245.5	17.8	523	4	US-09-270-767-25712	Sequence 25712, A
45	245.5	17.8	600	4	US-09-270-767-10334	Sequence 10334, A

ALIGNMENTS

RESULT 1
US-09-709-103-40
Sequence 40, Application US/09709103
Patent No. 6733991
GENERAL INFORMATION:
APPLICANT: Cismowski, Mary
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/709,103
CURRENT FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
LENGTH: 837
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(834)
OTHER INFORMATION:
US-09-709-103-40

Alignment Scores:

Pred. No.: 3.49e-180
Score: 1372.00
Percent Similarity: 99.62%
Best Local Similarity: 99.62%
Query Match: 99.64%
DB: 4
Gaps: 0

US-09-778-963B-2 (1-266) x US-09-709-103-40 (1-837)
Qy 1 MetMetlyThrIeuSerSerGlyAsnCyThrIeuSerValProAlaIysAsnSerTyr 20
Db 37 ATATGTAAGACTTTGTCTCAGCGGAACTGCACCTCAGTGTGCCGCAAAAATCTATAC 96

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QY      21 ArgMetValValIleuGlyValSerArgValIleYlySerSerIleValSerArgPheLeu 40
DB      97 CGCATGGTGTGGTGGGCTCTCGGGTGGCAAGAGCTCATCGTGTCTGCTTC 156
QY      41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluPhePheHisArgIlyValTyr 60
DB      157 AATGGCCGCTTTGAGGACGAGTACACACCCACCTTCAGGAGCTTCCACCGTAAGGTATAC 216
QY      61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB      217 AACATCCGCGCGACATGATACAGCTCGACATCTGGATCTCTGGCAACACCCCTTC 276
QY      81 ProIleMetArgArgIleSerIleLeuThrGlyAspValPheIleLeuValPheSerIleu 100
DB      277 CCGGCATGCGCAGGCTGCTCATCTCCACAGGGAGATGCTTCATCTGTGTTCAGCCCTG 336
QY      101 AspAsnArgGluSerPheAspGluValIlyArgIleuGlnIleuGlnValIlyAs 120
DB      337 GATTAACCGGAGTCTTCGATGAGTCAAGCCCTTCAGAACATCTCTGGAGGTCAAG 396
QY      121 SerCysLeuIlyAsnIlyThrIlyGlyValIleuValIleuProMetValIleCysGlyAsn 140
DB      397 TCTTGTCTGAGAACAGAACAGACCAAGAGGCGGAGAGTCCCATGTGTCATCTGTGGAC 456
QY      141 LysAsnAspHisGlyGlyLeuGlyAspGlnValProThrThrGluValIleuVal 160
DB      457 AAGAAACAGACCAAGCGAGCTGTGCGGCGGAGTCCACCAAGAGGCGGAGTGTG 516
QY      161 SerGlyAspGluAsnSerIleTyrPheGluValSerIleValIlyAsnThrAsnValAsp 180
DB      517 TCGGCGAGACAGAACTCGCCTTCACTTCAGAGTGTGCGGCGAAGAAACCAACAGTGGAC 576
QY      181 GluMetPheTyrValIleuPheSerMetAlaIlyLeuProHisGluMetSerProAlaLeu 200
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QY      201 HisArgIlyIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMetArg 220
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QY      221 ArgValIlyGluMetAspAlaTyrGlyMetValSerProPheAlaArgProSerVal 240
DB      697 CGCGTCAGAGAGATGACGCTCATGCGCATGATCTGCGCTTCGCGCCGCGCCAGCGTC 756
QY      241 AsnSerAspLeuIlyTyrIleValIlyValIleuArgGlnIlyGlnAlaArgGluArg 260
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QY      261 AspLysCysThrIleGln 266
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RESULT 2

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US-09-439-410A-40
; Sequence 40, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; TITLE OF INVENTION: Duzic, Emir
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(834)

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OTHER INFORMATION:

US-09-439-410A-40

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Pred. No.:	3,49e-180	Length:	837
Score:	1372.00	Matches:	265
Percent Similarity:	99.62%	Conservative:	0
Best Local Similarity:	99.62%	Mismatches:	1
Query Match:	99.64%	Indels:	0
DB:	4	Gaps:	0

US-09-778-963b-2 (1-266) x US-09-439-410A-40 (1-837)

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QY      21 ArgMetValValIleuGlyValSerArgValIleYlySerSerIleValSerArgPheLeu 40
DB      97 CGCATGGTGTGGTGGGCTCTCGGGTGGCAAGAGCTCATCGTGTCTGCTTC 156
QY      41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluPhePheHisArgIlyValTyr 60
DB      157 AATGGCCGCTTTGAGGACGAGTACACACCCACCTTCAGGAGCTTCCACCGTAAGGTATAC 216
QY      61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB      217 AACATCCGCGCGACATGATACAGCTCGACATCTGGATCTCTGGCAACACCCCTTC 276
QY      81 ProIleMetArgArgIleSerIleLeuThrGlyAspValPheIleLeuValPheSerIleu 100
DB      277 CCGGCATGCGCAGGCTGCTCATCTCCACAGGGAGTCTTCATCTGTGTTCAGCCCTG 336
QY      101 AspAsnArgGluSerPheAspGluValIlyArgIleuGlnIleuProMetValIleCysGlyAsn 120
DB      337 GATTAACCGGAGTCTTCGATGAGTCAAGCCCTTCAGAACAGATCTGTGAGGTCAAG 396
QY      121 SerCysLeuIlyAsnIlyThrIlyGlyValIleuValIleuProMetValIleCysGlyAsn 140
DB      397 TCTTGTCTGAGAACAGAACAGACCAAGAGGCGGAGTCCACCAAGAGGCGGAGTGTG 516
QY      141 LysAsnAspHisGlyGlyLeuGlyAspGlnValProThrThrGluValIleuVal 160
DB      457 AAGAAACAGACCAAGCGAGCTGTGCGGCGGAGTCCACCAAGAGGCGGAGTGTG 576
QY      161 SerGlyAspGluAsnSerIleTyrPheGluValSerIleValIlyAsnThrAsnValAsp 180
DB      517 TCGGCGAGACAGAACTCGCCTTCACTTCAGAGTGTGCGGCGAAGAAACCAACAGTGGAC 576
QY      181 GluMetPheTyrValIleuPheSerMetAlaIlyLeuProHisGluMetSerProAlaLeu 200
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QY      201 HisArgIlyIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMetArg 220
DB      637 CATCGAAGATCTCGGTGACATGACGATGACGCTTCACCCAGAGCCCTTCTGATGCGC 696
QY      221 ArgValIlyGluMetAspAlaTyrGlyMetValSerProPheAlaArgProSerVal 240
DB      697 CGCGTCAGAGAGATGACGCTCATGCGCATGATCTGCGCTTCGCGCCGCGCCAGCGTC 756
QY      241 AsnSerAspLeuIlyTyrIleValIlyValIleuArgGlnIlyGlnAlaArgGluArg 260
DB      757 AACAGTGACCTCAAGTACATCAAGGCCCAAGGTCTTCGCGAAGGCCAGGCCGCTGAGAG 816
QY      261 AspLysCysThrIleGln 266
DB      817 GACAAAGTGCAACATCCAG 834

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RESULT 3

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US-09-949-016-5022
; Sequence 5022, Application US/09949016
; Patent No. 6812339

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PABCSQ for Windows Version 4.0
; SEQ ID NO 5022
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5022

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Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
Gaps: 0

US-09-778-963b-2 (1-266) x US-09-949-016-5022 (1-837)

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Qy 21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db 97 CGCATGCTGTGCTGGGTGCTCTCGGTGGGCAAGACTCCATCTGTCTCGCTTCTC 156
Qy 41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgValTyr 60
Db 157 AATGGCCGCTTGGAGACAGTACACACCACCTCGAGACTTCCACCGTAAGTATAC 216
Qy 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
Db 217 AACATCGCGCGCATGTACCACTGCACTCTGATACCTTGACCAACACCCCTTC 276
Qy 81 ProAlaMetArgTyrLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
Db 277 CCGCCATGCGCAGGCTGTCTCATCTCCACAGGGATGTCTTCACTCTGTGTTCAGCTG 336
Qy 101 AspAsnArgGluSerPheAspGluValValArgLeuGlnGlyGlnIleLeuGluValLys 120
Db 337 GATTAACGGGAGTCTCTCATGAGTCAAGCGCTTCAAGAGCAGATCTTGAAGTCAAG 396
Qy 121 SerCyAlaLeuValAsnValThrValGluAlaIleGluLeuProMetValIleCyArgGlyAsn 140
Db 397 TCCGCTGTGAAGCAAGAACAGAGAGCGGCGAGCTGCCATGCTGTGCGGCAAC 456
Qy 141 LysAsnAspHisGlyGluLeuCyArgGlnValProThrThrGluAlaGluLeuVal 160
Db 457 AAGAACACACACCGCGAGCTGTGCCCGCAGTGTCCACACCGAGCGCGAGCTGTG 516
Qy 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaValAsnThrAsnValAsp 180
Db 517 TCGGCGACAGGAGACTGCGCTTCAAGAGTGTGCGCAAGAGAACACCAAGTGTGAC 576
Qy 181 GluMetPheTyrValIleuPheSerMetAlaValLeuProHisGluMetSerProAlaLeu 200
Db 577 GAGATGTTTCAAGTCTTTCAGCATGTGCCAAGCTGCACACGAGAGAGCGCCGCTG 636
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Db 637 CATGCAAGATCTCCGTGACGATACGAGCTTCCACCCAGGCGCTTCTGCATGCGC 696
Qy 221 ArgValValGluMetAspAlaTyrGlyMetValSerProPheAlaArgProSerVal 240
Db 697 CGGCTCAAGAGATGACGCGCTTATGAGTGTCTGCGCTTCCGCCGCCCGCAGGCTC 756
Qy 241 AsnSerAspLeuValTyrIleValAlaValLeuArgGluGlyGlnIleArgGluArg 260
Db 757 AACGATCCTCAAGTACATCAACGCGCAAGGCTCTTGGAAAGCCAGCGCCGTGAGAG 816
Qy 261 AspLysCyThrIleGln 266
Db 817 GACAGTGCACCATCCAG 834

RESULT 4
US-09-949-016-16764
; Sequence 16764, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PABCSQ for Windows Version 4.0
; SEQ ID NO 16764
; LENGTH: 9259
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16764

Alignment Scores:
Pred. No.: 1,73e-114 Length: 9259
Score: 911.00 Matches: 176
Percent Similarity: 98.33% Conservative: 1
Best Local Similarity: 97.78% Mismatches: 3
Query Match: 66.16% Indels: 0
Gaps: 0

US-09-778-963b-2 (1-266) x US-09-949-016-16764 (1-9259)

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Db 6717 TCTCTCCCTGACAGGGAGTGTCTTCACTCTGTGTTCAGCTGTGAATACCGGAGTCTTC 6776
Qy 107 AspGluValValArgLeuGlnGlyGlnIleLeuGluValLysSerCyAlaValAsnLys 126
Db 6777 GATGAGTCAAGGCGCTTCAAGAGCAGATCTGAGGTCAAGTCTTCTGAAAGAACAG 6836
Qy 127 ThrLysGluAlaIleGluLeuProMetValIleCyArgGlyAsnValAsnAspHisGlyGlu 146
Db 6837 ACCAAGAGGCGGCGAGCTGCCCATGTGTATCTGTGTGCAACAAAGACACAGCGGAG 6896
Qy 147 LeuCyArgGlnValProThrThrGluAlaGluLeuValSerGlyAspGluAsnSer 166
Db 6897 CTGTGCGCCAGGTGTGCCACACCGAGCGAGCTGTGTGTGCGGCGAGCAAGACTGC 6956
Qy 167 AlaTyrPheGluValSerAlaValAsnThrAsnValAspGluMetPheTyrValLeu 186
Db 6957 GCCTTACTCGAGGTGTGCGGCAAGAGAACACCAAGTGTGATCTTACGTCGCTC 7016
Qy 187 PheSerMetAlaValLeuProHisGluMetSerProAlaLeuHisArgValIleSerVal 206
Db 7017 TTCAGATGTGCAAGCTGTGCACAGAGATGAGCCCGCCCTGTGATGCAAGATCTCGCTG 7076
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QY 61 AsnIleArgIYAspMetTYrGlnLeuAspIleLeuAspThrSerGIYAsnHISProPhe 80
Db 196 TCATTCGGCGGCGAGGTCTACAGCTCCGACATCTCCGACAGTCCGGCAACACCCGTTCC 255
QY 81 ProIaMetArgATGLeuSerIleLeuThrGIYAspValPheIleLeuValPheSerLeu 100
Db 256 CCCGCATCGCGCGCTCTCCATCTCTCACAGAGAGCGTTTTCATCTCTGTGTCAGTGTG 315
QY 101 AspAsnArgIYAspMetPheAspGluValIYAspArgLeuGlnIYAspGlnIleLeuGluValIYAs 120
Db 316 GACAAACCGGCACTCTCTTCAGAGAGGTGACGCGCTCAGGACGATCTTCCGACCAAG 375
QY 121 SerCysLeuLYAsnLYThrLYGlnLYIleLYAspLYValIleLYGlnLYLeuLYProLYMetLYValIleCYsGIYAsn 140
Db 376 TCTTGCTCTCAAGAACAAACCAAGAGAACGTGACGTCCTCCCTGTATCTGCGGCAAC 435
QY 141 LYAsnAspPheIleGIYLeuLYCysArgGlnValIleProThrThrGlnIleValIleLeuValI 160
Db 436 AAGGTGACCGC---GACTTCTACCGCGAGGTGACGACCGCGAGATCGACAGCTGTTG 492
QY 161 SerGIYAsp---GluAsnSerIleATyrPheGluValSerIleAlaLYIleLYAsnValI 179
Db 493 GCGCAGCAACCCCGCGCTGCGCTGCTGAGATCTCGCGCAAGAACAGACAGCTGTG 552
QY 180 AspGluMetPheTYrValIleuPheSerMetAlaLYIleuProHISGluMetSerProIa 199
Db 553 GACCAAGATGTTCCGCGCGCTCTTGGCCATGCGCAAGCTGCCAGGAGATGAGCCCAAC 612
QY 200 LeuHISArgLYIleSerValGlnTYrGIYAspAlaPheHISProArgProPheCysMet 219
Db 613 CTGACCGCGCAAGGTCTCGGTGACAGTACTGCAACGCTGCAAGAG-----GCGCTG 666
QY 220 ArgArgValIYAspGluMet-----AspAla 227
Db 667 CGGAACAAGAGCTGCTGCGGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 726
QY 228 TYrGIYMetValSerProPheAlaArgArgProSerValIleAsnSerAspLeuLYrIle 247
Db 727 TTTGGCATCTGGGACCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 786
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Db 787 CGCGAAGAGCG 840
RESULT 7
US-09-709-103-45
; Sequence 45, Application US/09709103
; Patent No. 673391
; GENERAL INFORMATION:
; APPLICANT: Cisnowski, Mary
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709, 103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (146)..(988)
; OTHER INFORMATION:
US-09-709-103-45
Alignment Scores:
Pred. No.: 3,03e-111 Length: 1740
Score: 879.00 Matches: 172
Percent Similarity: 77.70% Conservative: 44
Best Local Similarity: 61.87% Mismatches: 46
Query Match: 63.83% Indels: 16

DB: 4 Gaps: 4
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Db 161 ATGATCAAGAGATGTGCTCCGAGGACTCCGAGGTGAGTATCCGCGCAAGAACTGCTAT 220
QY 21 ArgMetValIleLeuGlnIleAspArgValIYLYsSerSerIleValSerArgPheLeu 40
Db 221 CGCATGTCTATCTCTCGGCTGCTCCAGGTGGGCAAGCGGCATCTGTGCGCTTCTC 280
QY 41 AsnGIYArgPheGluAspGlnTYrThrProThrIleGluAspPheHISArgLYrValTYr 60
Db 281 ACCGCGCGCTTCAGAGACGCTTACAGCTTACCTTCCAGAGACTTCCACCGCACTTAC 340
QY 61 AsnIleArgIYAspMetTYrGlnLeuAspIleLeuAspThrSerGIYAsnHISProPhe 80
Db 341 TCATTCGCGCGGAGGTCTACAGCTCGACATCTCGACAGCTCCGCGCAACACCGTTTC 400
QY 81 ProIaMetArgATGLeuSerIleLeuThrGIYAspValPheIleLeuValPheSerLeu 100
Db 401 CCCGCATCGCGCGCTCTCCATCTCCACAGAGACGTTTTCATCTGTGTTGACTGTG 460
QY 101 AspAsnArgIYAspMetPheAspGluValIYAspArgLeuGlnIYAspGlnIleLeuGluValIYAs 120
Db 461 GACAAACCGCACTCTTCAGAGAGTCAAGCGCTCAGGACGATCTCTGACACCAAG 520
QY 121 SerCysLeuLYAsnLYThrLYGlnLYIleLYAspLYValIleLYGlnLYLeuLYProLYMetLYValIleCYsGIYAsn 140
Db 521 TCTTGCTCTCAAGAACAAACCAAGAGAACGTGACGTCCTCCCTGTATCTGCGGCAAC 580
QY 141 LYAsnAspPheIleGIYLeuLYCysArgGlnValIleProThrThrGlnIleValIleLeuValI 160
Db 581 AAGGTGACCGC---GACTTCTACCGGAGGTGACCGCGCGAGATCGAGAGCTGTG 637
QY 161 SerGIYAsp---GluAsnSerIleATyrPheGluValSerIleAlaLYIleLYAsnValI 179
Db 638 GCGCAGCAACCCCGCGCTGCGCTGCTTGAAGTCTCGGCAAGAACAGACGCTG 697
QY 180 AspGluMetPheTYrValIleuPheSerMetAlaLYIleuProHISGluMetSerProIa 199
Db 698 GACCAAGATGTTCCGCGCGCTCTTGGCCATGCGCAAGCTGCCAGGAGATGAGCCCAAC 757
QY 200 LeuHISArgLYIleSerValGlnTYrGIYAspAlaPheHISProArgProPheCysMet 219
Db 758 CTGACCGCGCAAGGTCTCGGTGACAGTACTGCGAGCTGTGCAAGAG-----GCGCTG 811
QY 220 ArgArgValIYAspGluMet-----AspAla 227
Db 812 CGGAACAAGAGCTGCTGCGGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 871
QY 228 TYrGIYMetValSerProPheAlaArgArgProSerValIleAsnSerAspLeuLYrIle 247
Db 872 TTTGGCATCTGGGACCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 931
QY 248 LYAsnAlaLYValLeuArgGlnGlnIleAlaArgIYAspLYrIle 265
Db 932 CGCGAAGAGCG 985
RESULT 8
US-09-439-410A-45
; Sequence 45, Application US/09439410A
; Patent No. 674682
; GENERAL INFORMATION:
; APPLICANT: Cisnowski, Mary
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEOTIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439, 410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1

Db	706	GACCGAGATGTTCCGGCGCGCTCTTCCGCATGGCCAAAGCTGCCAGGAGATGAGCCCAAG	765
Qy	200	LeuH1aArgLySLeSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet	219
Db	766	CTGCACCCGCAAGTGTCTCGGTGCAGTACTGCGACGTCGTCGACAAAG-----CGCGTG	819
Qy	220	ArgArgValLySGLuMet-----AspAla	227
Db	820	CGGAACAAGAACCTCTCGCGGCGCGGACCGCGCGCGCGCGGACCCGGCGGACCCG	879
Qy	228	TyrGlyMetValSerProPheAlaArgArgProSerValAanSerAspLeuTyrIle	247
Db	880	TTTGGCATCTGTGGCACCTTTCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG	939
Qy	248	LySAlaLySValLeuArgGLuGlyGlnAlaArgGluArgAspLySCysThrIle	265
Db	940	CGCGAAGAGCGCCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	993
RESULT 10			
US-09-439-410A-3			
; Sequence 3, Application US/09439410A			
; Patent No. 6746852			
; GENERAL INFORMATION:			
; APPLICANT: Cismowski, Mary			
; INVENTOR: Duzic, Emil			
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEOTIC ACID MOLECULES AND USES THEREOF			
; FILE REFERENCE: 1919/60388-B			
; CURRENT APPLICATION NUMBER: US/09/439,410A			
; CURRENT FILING DATE: 1999-11-11			
; NUMBER OF SEQ ID NOS: 118			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 3			
; LENGTH: 1801			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (154)..(996)			
; OTHER INFORMATION:			
US-09-439-410A-3			
Alignment Scores:			
Pred. No.: 3,216-111 Length: 1801			
Score: 879.00 Matches: 172			
Percent Similarity: 77.70% Conservative: 44			
Best Local Similarity: 61.87% Mismatches: 46			
Query Match: 63.83% Indels: 16			
DB: 4 Gaps: 4			
US-09-778-963B-2 (1-266) x US-09-439-410A-3 (1-1801)			
Qy	1	MetMetLySThrLeuSerSerGlyAlaSerGlyThrLeuSerValProAlaLyAsnSerTyr	20
Db	169	ATGATCAAGAAGATGATGCGCCGAGCAATCTCGAGCTGAGATATCCGGCCAAAGATGCTAT	228
Qy	21	ArgMetValIleValLeuGlyAlaSerArgValGlyLySerSerIleValSerArgPheLeu	40
Db	229	CGCAATGCTCATCTCGGCTCGGCTCGGCAAGGTGGGCAAGAGCGGCATGTCTCCGCTCTC	288
Qy	41	AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLyValTyr	60
Db	289	ACCGGCGCGCTTCGAGAGCGCCCTACAGCGCTTACATCGAGGACTTCCACCGCAAGTTCTAC	348
Qy	61	AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe	80
Db	349	TCCATCTCGGCGGAGGTCTTACAGGCTGCACATCTTCGACAGTCCGGGCAACCCCGTTC	408
Qy	81	ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu	100
Db	409	CCCGGCAATGCGGCGCGCTCTCCATCTCTCAACAGAGACGTTTTCATCTCTGTTCAGTCTG	468
Qy	101	AspAsnArgGluSerPheAspGluValLySArgLeuGlnLySGLuIleLeuGluValLyS	120

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Db      469  GACAAACCGGACATCTCTTCAGAGAGGTGACGCCGCTCAGGACAGATCTTGACACCAAG 528
Qy      121  SerCysLeuYsaAnbYrThrLySgluaIaAgluLeuProMetValIleCySgLYasn 140
Db      529  TCTTGGCTCAAGAAACAAAACCAAGAGGAACGTGACAGTGGCCCTGTGATCTGGCGGAC 588
Qy      141  LysAsnAspHisSglYgluLeuCySvArglnValProThrThrGluuAgluLeuVal 160
Db      589  AAGGTGACCGC---GACTTCTACCGCCGAGGTGACCAAGCGAGATGACAGCTGTGTG 645
Qy      161  SerGlyAsp---GluAsnSerIaTrYPheGluValSerAlaLysLysAsnThrAsnVal 175
Db      646  GCGACACACCCCAAGCGCTGCGCTTACTTCGAGATCTGGCCCAAGAAACAGCAGCTTG 705
Qy      180  AspGluMetPheTrValLeuPheSerMetAlaLysLeuProHisSgluMetSerProAla 195
Db      706  GACCAAGATGTTCCGGCGCGCTCTTCCGCAGATGCGCAAGCTGCCCAAGAGATAGCCCAAG 765
Qy      200  LeuHisArgLysLysSerValGlnTrGlyAspAlaIleHisIleProArgProPheCysMet 215
Db      766  CTGACACCGCAAGGTCTCGGTGACGATGTCGACGTGCTGCACAAGAG-----GCGCTG 813
Qy      220  ArgArgValLysGluMet-----AspAla 222
Db      820  CGAACAAGAAAGTGTGTGCGGGCCGAGCGGCGGCGGCGGCGGACCCGGCGGACGCC 875
Qy      228  TyrGlyMetCysSerProPheAlaArgArgProSerValAsnSerAspLeuLysTrIle 247
Db      880  TTGGGATCGTGGCACCTTCCGCGCGCGCGCCACGCAACAGCAAGCACTCATATCATC 933
Qy      248  LysAlaLysValLeuArgGluGlnAlaArgGluArgAspLysCysThrIle 265
Db      940  CGCGAAGAGGCGCAGCGCGCGGACGACAGGCGCAAGAGCAGAGCGCTGGCTCATC 993

RESULT 11
US-09-053-374A-1
: Sequence 1, Application US/09053374A
: Patent No. 6462177
: GENERAL INFORMATION:
: APPLICANT: YEN, KWANG-MU
: TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: AMGEN INC.
: STREET: ONE AMGEN CENTER DRIVE
: CITY: THOUSAND OAKS
: STATE: CA
: COUNTRY: US
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/053,374A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: COOK, ROBERT R.
: REGISTRATION NUMBER: 31,602
: REFERENCE/DOCKET NUMBER: A-514
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1841 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 255..1097

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US-09-053-374A-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
3.33e-111	879.00	1841	172
Percent Similarity:	77.70%	Conservative:	44
Best Local Similarity:	61.87%	Mismatches:	46
Query Match:	63.83%	Indels:	16
DB:	3	Gaps:	4

US-09-778-963B-2 (1-266) x US-09-053-374A-1 (1-1841)

```

QY 1 MetMetlyrThrLeuSerSerGlyAncySthrLeuSerValProAlaIlyAsnSerTyr 20
DB 270 ATGATCAAGAAAGATGTGCGCGAGCTACGAGCTGAGTATCCGCGCCAAAGATCTCTAT 329
QY 21 ArgMetValIleuGlyAlaSerArgValGlyLySerSerIleValSerArgPheLeu 40
DB 330 CGCATGTGATCTCTCGGCTGCTCCCAAGGTGGCAAGCGCCATCTGTCCGCTTCTC 389
QY 41 AsnGlyArgPheGluAspGlnTyrThrProThriIleGluAspPheIAsrGlyValTyr 60
DB 390 ACCGCGCGCTTCGAGGAGCGCTACAGCTTACATCGAGGCTTCCACCGCAAGTTCTAC 449
QY 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB 450 TCCATCCCGCGGAGGTCTACAGCTCGACATCTCGACAGCTCCGGAACACCCGCTTC 509
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
DB 510 CCGCGCATGCGCGCGCTCTCCATCTCCAGAGAACGTTTCATCTCGGTTCAGTCTG 569
QY 101 AspAsnArgGluSerPheAspGlnValIlyAsrGleuGlnIlySerGlnIleGluValIly 120
DB 570 GACACCGCGGAGCTCTTCGAGAGGTGAGCGGTACGAGCAGCATCTTCAGACACAG 629
QY 121 SerCysLeuIlyAsnIlyThrIlyGlnAlaIAsgluLeuProwetValIleCysGlyAsn 140
DB 630 TCTTGCTCCAGAAACAAACCAAGAGAACCGTCGACGCGCTTCATCTCGCGGCAAC 689
QY 141 LysAsnAspHisGlyGlnLeuGlyAsrGlnValPProThrThrGlnAlaGlnLeuLeuVal 160
DB 690 AAGGTGACCGC---GACTTCTACCGCGAGGTGACACAGCGCGGATCGAGCTGTGT 746
QY 161 SerGlyAsp---GluAsnSerAlaTyrPheGlnValSerAlaIlyAsnIlyAsnThrAsnVal 179
DB 747 GCGCAGCAGCCCGCGCGCTGCGCTTCTGAGATCTCGGCCAAGAACAGACAGCTGT 806
QY 180 AspGlnMetPheTyrValIleuPheSerMetAlaIlyLeuProHisGluMetSerProAla 199
DB 807 GACCAAGATGTTCCCGCGGCTCTTCGCGCATGGCCAAAGCTGCCAGCGAGATGACCCAGAC 866
QY 200 LeuHisArgIlySeriLeuSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet 219
DB 867 CTGACCGGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 920
QY 220 ArgArgValIlyGlnLeuT---AspAla 227
DB 921 CGGAAACAAAGAGCTGCTGCGCGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 980
QY 228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuIlyTyrIle 247
DB 981 TTTGGCAGTCGTGGACCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1040
QY 248 LysAlaIlyValIleuArgGlnGlyGlnAlaArgGlnIlyAspIlySerCysThrIle 265
DB 1041 CGCGAGAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCTATC 1094

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RESULT 12

US-09-053-374A-4
 ; Sequence 4, Application US/09053374A
 ; Patent No. 6462177
 ; GENERAL INFORMATION:

```

APPLICANT: YEN, KWANG-MU
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: US
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 132..971
US-09-053-374A-4
Alignment Scores:
Pred. No.: 6.41e-111 Length: 1689
Score: 876.50 Matches: 171
Percent Similarity: 77.98% Conservative: 45
Best Local Similarity: 61.73% Mismatches: 46
Query Match: 63.65% Indels: 15
DB: 3 Gaps: 4
US-09-778-963B-2 (1-266) x US-09-053-374A-4 (1-1689)
QY 1 MetMetlyrThrLeuSerSerGlyAncySthrLeuSerValProAlaIlyAsnSerTyr 20
DB 147 ATGATCAAGAAAGATGTGCGCGAGCTACGAGCTGAGTATCCGCGCCAAAGATCTGCTAC 206
QY 21 ArgMetValIleuGlyAlaSerArgValGlyLySerSerIleValSerArgPheLeu 40
DB 207 AGGATGTGATCTCTCGCTCATCCAAAGTGGCAAGCGCGCATCTGTCCGCTTCTC 266
QY 41 AsnGlyArgPheGluAspGlnTyrThrProThriIleGluAspPheIAsrGlyValTyr 60
DB 267 ACGGCGCGCTTCGAGGAGCTTACACCCCTTACATTGAAGCTTCCACCGAAAGTTTAC 326
QY 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB 327 TCGATCCCGCGGAGAGCTTACCAAGTGGACATCTGACACATCTGCAATCATCCGCTT 386
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
DB 387 CCGCGCATGCGCGCGCTCTCTATCTCATCAGAGAGACCTTTTCTATCTGCTGCTTCACTTCA 446
QY 101 AspAsnArgGluSerPheAspGlnValIlyAsrGleuGlnIlySerGlnIleGluValIly 120
DB 447 GACAAACCGGAGCTCTTCGAGAGAGTGCAAAGGCTCAACAGCAGATCTAGACACCAAG 506
QY 121 SerCysLeuIlyAsnIlyThrIlyGlnAlaIAsgluLeuProwetValIleCysGlyAsn 140
DB 507 TCTGTCTCAAGAAACAAACCAAGAGATGTGACGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 566

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OY      141  LVVAASAAAPHN1ESGLVLEUCYSVA3SGINValProthrhrglu1agi1u1e1u1Val 160
Db      567  AAAGGGAGCCGG---GACTTCTACCGGAAGTGAAGACGGGAGATTGACAGCTGGTG 623
OY      161  SerGIyAp---GluAmsSerAlaTyPheGluValSerAlaLysLVSAenThAsnVal 179
Db      624  GCGAGTAGACCCCTACAGCGTTGTGCTCTACTTGAAATCTCGGCCAAGAAATTAAGAGCTTG 683
OY      180  AapGIuMeCPhetyrValLeuPheSerMetAlaLysLeuProH1eGIuMeCSePProAla 199
Db      684  GACCAAGATGTCGTCGTCGCTCTTGCCATGCGCAAGCTGCTGACGAGTAAGACCCCTGAC 743
OY      200  LeuH1aArGLyL1eSerValG1nTyrg1aYAspAlaPheH1aProAapPProPheCyMeC 219
Db      744  TTGCACCGGAAGGTCTCTGTGCACTACTGTGAAGCTGCTGCACAAAGA-----GCTCTG 797
OY      220  ArGaRgValLySGluMeC-----AspAlaTyR 228
Db      798  AGGAACAAGAGCTTCTGCGTGCGGCGACGCGAGGTGGGGGCGACACGAGATGCGCTTT 855
OY      229  G1yMeCValSerProPheAlaArGaRgProSeRValAmsSerAspLeuLyTyR11eLys 248
Db      858  GGCATCTTGCGCGCCCTTGTCTCCACAACCTAAGCGTGATGACCACTCATGTCATTCGT 917
OY      249  AlA1yVValLeuArGLyG1uG1yG1nAlaArGGLuAaRgAspLyCySeThr11e 265
Db      918  GAGAAACCAAGTGTCACGACCGCAGGCTTAAGACAAAGAGCGCTGTGTCAATC 968

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RESULT 13
US-09-053-374A-6
: Sequence 6, Application US/09053374A
: Patent No. 6462177
: GENERAL INFORMATION:
: APPLICANT: YEN, KWANG-MU
: TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: AMGEN INC.
: STREET: ONE AMGEN CENTER DRIVE
: CITY: THOUSAND OAKS
: STATE: CA
: COUNTRY: US
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/053,374A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: COOK, ROBERT R.
: REGISTRATION NUMBER: 31,602
: REFERENCE/DOCKET NUMBER: A-514
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3079 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-053-374A-6

Alignment Scores:
Pred. No.: .
Score: 1,2e-102
Percent Similarity: 820.00
Best Local Similarity: 66.56%
Query Match: 52.63%
DB: 5,55%
Length: 3079
Matches: 170
Conservative: 45
Mismatch: 47
Indels: 62
Gaps: 5

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US-09-778-963B-2 (1-266) x US-09-053-374A-6 (1-3079)

QY	1	MethelytrhLeuSerSerGlyAsnCyethrLeuSerValProAlalybAnSerTyr	20
Db	318	ATGATCAAGAAAGATGGTCCCAAGGACCTGMACTGAGTATCCGGCCAAAGACTGCTAC	377
QY	21	ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu	40
Db	378	AGATGGTCATCTTCGGCTCATCCAAAGTGGGCAAGACGGSCATCGTCCGCTTCTC	437
QY	41	AsnGlyArgPheGluArgSerGlnTyrThrProThrIleGluArgPheH1bArgLysValTyr	60
Db	438	ACGGGCGCGCTTCAGAGACGGCTTACACCCCTTACCATTAAGACTTCCACCGAAATGTTTAC	497
QY	61	AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnH1aProPhe	80
Db	498	TCGATCCGCGCGGCAAGCTTACCACTGTGAACATCTGGACACATCTGGCAATCATCCGTTT	557
QY	81	ProAlaMetArgArgLysLeuSerIle	88
Db	558	CCCCCATGGCGCGCTCTCTATCTCACAAGTGAAGTGGGGACCCGACAGGACCGGTGG	617
QY	88	-----	88
Db	618	GAGGGAATCTGCGGGAGACGGATGGGCGGNGTGTGTGCTTGGGCGCTGCTCTCTCT	677
QY	89	-----LeuThrGlyAspValPhe	94
Db	678	GCTCCGCTGGTGGACGCTGCCCTCACCCTTTCACCTGCTCCCTTGTGA-GAGAGGTTTTC	736
QY	95	IleLeuValPheSerIleAspAsnArgGlyLysSerPheAspGluValLysArgLeuGlnLys	114
Db	737	ATTCTGGTGTTCACCTTATGACACACCGGACCTCTTCGAGAGAGTGCAAAGGCTCAAAACAG	796
QY	115	GlnIleLeuGluValLysSerCysLeuLysAsnLysThrLysGluAlaIleGluLeuPro	134
Db	797	CAGATCCTAGACACCAAGTCCCTGCTCAGAACAAACCAAAAGAAATGTGACAGTCCG	856
QY	135	MetValIleCysGlyAsnLysAsnAspH1bGlyLysLeuCysArgGluValProThrThr	154
Db	857	CTGGTCATTTGGCGGTAAACAAAGGGGACCGG--GACTTCTACCGCGAAATGTGACAGCGG	913
QY	155	GluAlaGluLeuLeuValSerGlyAsp---GluAsnSerAlaTyrPheGluValSerAla	173
Db	914	GAGATTAGACAGCTGCTGGCGGAGACCTTCAGCGTTGTGCTACTTCGAGATCTCGGCC	973
QY	174	LysLysAsnThrAsnValAspGluMetPheTyrValLeuPheSerMetAlaLysLeuPro	193
Db	974	AAAGAAATAGACACCTGCACCAAGATGTCGCTGCGCTCTTGGCCATGGCCAAAGCTCCT	1033
QY	194	H1bGluMetSerProAlaLeuH1aArgLysIleSerValGlnTyrGlyAspAlaPheH1b	213
Db	1034	AGCAGAGATGACCCCTGACTGTGACCGGAAAGGTGTCTGTGACATCTGTGACGTGCTGCAC	1093
QY	214	ProArgProPheCysMetArgArgValLysGluMet-----	225
Db	1094	AAAAAG-----GCTCTGAGGAACAAGACTTCTGCGTCCGGGCAACGAGCGGGGGC	1147
QY	226	-----AspAlaTyrGlyMetValSerProPheAlaArgArgProSerValAsnSer	242
Db	1148	GACCAACGAGATGCGCTTGGGATCTTGGCGCCCTTCTGCGACAGACTTAAGGTGTCATAGC	1207
QY	243	AspLeuLysTyrIleLysValLysValLeuArgGluLysGlnIleArgGluArgAspLys	262
Db	1208	GACCTCATGTACATTTCGAGAAAAACAAGTGTACAGACCAAGGCTTAAGACAAAGGAGCGC	1267
QY	263	CyethrIle	265
Db	1268	TGTGTCAATC	1276

RESULT 14
US-09-053-374A-3

Job time : 216 secv

Db	2918	ATGATCAAGAAAGATGTGCCCGGACGACCTCGAGCTCGAGTATTCGCCGCAAGAACTGCTAT	2977
Qy	21	ArgMetValIvalLeuGlyAlaSerArgValGlyIysSerSerIleValSerArgPheLeu	40
Db	2978	CGCATGTGTCATCTCTCGGCTCGCTGCCAAGGTGGGCAAGACGGGCATGTCTCCGCTTCTC	3037
Qy	41	AenGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgIleValTyr	60
Db	3038	ACCGGCCCCCTTCGAGGAAGCCCTACACGGCTTACATCGAGACTTCACCGCAAGTTCTAC	3097
Qy	61	AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe	80
Db	3098	TCGATCCCGCGGAGAGTCTACAGCTCGACATCTTCGACACGTCCGGCAACACCCGTTCC	3157
Qy	81	ProAlaMetArgArgLeuSerIleLeuThr	90
Db	3158	CCCGCGCATGCGGCGCTCTCCATCTCTACAGGTAGCCGGGGCCGGGCAAGTCGGGAG	3217
Qy	90	-----	90
Db	3218	GGAAAGGCGGGGAACTTCGGCGAGGGCGCCCGGACGCGGTCCGGCTCGCGCGGC	3277
Qy	90	-----	90
Db	3278	CGAGTAGTGCCTTGGCGCTTAGAGAGGCTAGCGCGCCCGCGGCTCAAAGTCAGCC	3337
Qy	90	-----	90
Db	3338	CGACTTGTCCCTGGGCGGCACTCTCACTTCTCTTTCGTGCTCTGTGCCCCCTCT	3397
Qy	91	-GlyAspValPheIleLeuValPheSerLeuAspAsnArgIleuSerPheAspGluValIy	110
Db	3398	AGGAGACCTTTTCATCTCGTGTTCAGTCTGGACAAACCGCACTCTTCGAGAGGTGCA	3457
Qy	110	SArgLeuGlnIysGlnIleLeuGluValIysSerCysLeuIysAsnIySThrIysGluAl	130
Db	3458	CGCGTTCAGGCGAGCATCTCTGACACCAAGTCTTGCTCAAAGAACAAACAGAGGAA	3517
Qy	130	AAAGluLeuProMetValIleCysGlyAsnIysAsnAspHisGluIleuLeuCysArgG1	150
Db	3518	CGTGACGCGCCCCGTGTCATCTGCGGCAACAAAGGTGACCGC--GACTTCTACCGGCA	3574
Qy	150	nValProThrThrGluAlaGluLeuLeuValSerGlyAsp--GluAsnSerAlaIyRph	169
Db	3575	GGTGACCAAGCGCGGATCGAGCACTGTGTGGCGACCAACCCCAAGCGCTCGCTACTT	3634
Qy	169	EGluValSerAlaIySlyAsnThrAsnValAspGluMetPheTyrValLeuPheSerMe	189
Db	3635	CGAGATCTTCGGCCAAAGAAAGACAGAGCCTGGACCAAGTGTTCGCGGCTTTCGCCAT	3694
Qy	189	CAIAlaLeuProHisGluMetSerProAlaLeuHisIAspIyValIeserValGlnTyrG1	209
Db	3695	GGCCAAAGCTGCCACAGAGATGAGCCAGACTCGACCGCAAGGCTCTGATGCAATAGT	3754
Qy	209	YAspAlaPheHisProArgProPheCysMetArgArgValIySGluMet-----	225
Db	3755	CGACTGTGTCGACAGAAAG-----GCCTGGGAAACAAAGAGCTGCTCGCGGCGGAG	3808
Qy	226	-----AspAlaTyrGlyMetValSerProPheAlaArgAr	237
Db	3809	CGGCGGCGGCGGCGGACCGCGGCGAGCGCTTTTGACATCGTGGACACCTTCGGCGCG	3868
Qy	237	gProSerValAsnSerAspLeuIyTyrIleValAlaIyValLeuArgIuGluGlnAl	257
Db	3869	GCCGCGCTACACAGCGACTCATGATCATCGCGAAGAGCGACGCGCGGACGACAGCG	3928
Qy	257	aArgGluArgAspIySyrCysThrIle	265
Db	3929	CAAGGACAAGAGCGCTCGTCTATC	3953

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2005, 05:50:40 ; Search time 631 Seconds

(without alignments)
2559.270 Million cell updates/sec

Title: US-09-778-963b-2

Perfect score: 1377
Sequence: 1 MMKTLSSGNCTLSVPAKNSV.....IKAVLREGQAREDKCTIQ 266

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QPM=fastlap -SUFPM=tmpp -MINMATCH=0.1
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Database :

Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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22: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1377	100.0	3082	9 US-09-778-963A-1	Sequence 10, Appl1
2	1372	99.6	837	18 US-10-804-491-40	Sequence 41, Appl1
3	1372	99.6	2832	10 US-09-918-715-174	Sequence 174, Appl
4	1372	99.6	2832	17 US-10-185-035-14	Sequence 4, Appl1
5	1372	99.6	2832	18 US-10-474-794-174	Sequence 174, Appl
6	1372	99.6	2973	10 US-09-918-715-197	Sequence 197, Appl
7	1372	99.6	2973	18 US-10-474-794-197	Sequence 197, Appl
8	1372	99.6	3058	18 US-10-723-860-514	Sequence 5134, Ap
9	1304	94.7	3020	18 US-09-918-715-292	Sequence 292, App
10	1304	94.7	3020	18 US-10-474-794-292	Sequence 292, App
11	911	66.2	11221	9 US-09-778-963A-3	Sequence 3, Appl1
12	911	66.2	16000	17 US-10-185-035-11	Sequence 11, Appl1
13	911	66.2	114771	18 US-10-723-860-458	Sequence 458, App
14	902	65.5	696	18 US-10-029-386-20951	Sequence 20951, A
15	879	63.8	846	18 US-10-804-491-1	Sequence 1, Appl1
16	879	63.8	1740	18 US-10-804-491-45	Sequence 45, Appl1
17	879	63.8	1744	14 US-10-197-666A-87	Sequence 87, Appl1
18	879	63.8	1801	18 US-10-804-491-3	Sequence 3, Appl1
19	586	42.6	1021	17 US-10-321-039-13	Sequence 13, Appl1
20	569	41.3	523	17 US-10-185-035-12	Sequence 12, Appl1
21	511	37.1	753	13 US-10-027-632-25123	Sequence 25123, A
22	511	37.1	753	13 US-10-027-632-25124	Sequence 25124, A
23	511	37.1	753	13 US-10-027-632-25125	Sequence 25125, A
24	511	37.1	753	17 US-10-027-632-25123	Sequence 25123, A
25	511	37.1	753	17 US-10-027-632-25124	Sequence 25124, A
26	511	37.1	753	17 US-10-027-632-25125	Sequence 25125, A
27	464	33.7	368	9 US-09-864-761-21643	Sequence 21643, A
28	373	27.1	405	9 US-09-860-352-10273	Sequence 10273, A
29	344	25.0	1108	15 US-10-037-270-945	Sequence 945, App
30	344	25.0	1108	17 US-10-117-722-945	Sequence 945, App
31	344	25.0	3061	18 US-10-363-829-290	Sequence 290, App
32	344	25.0	4167	18 US-10-399-455-36	Sequence 36, Appl1
33	343.5	24.9	3440	18 US-10-723-860-8287	Sequence 8287, Ap
34	341	24.8	597	10 US-09-873-546-4	Sequence 4, Appl1
35	341	24.8	597	16 US-10-029-386-22936	Sequence 22936, A
36	319	23.2	1249	18 US-10-363-829-77	Sequence 77, Appl1
37	300	21.8	2223	17 US-10-344-404-22	Sequence 22, Appl1
38	297	21.6	1733	16 US-10-096-534-66	Sequence 66, Appl1
39	297	21.6	1733	17 US-10-231-956A-428	Sequence 428, App
40	296	21.5	1504	14 US-10-197-666A-81	Sequence 81, Appl1
41	296	21.5	2297	18 US-10-322-281-473	Sequence 473, Appl1
42	296	21.5	2340	15 US-10-106-698-1073	Sequence 1073, Ap
43	296	21.5	2624	15 US-10-084-817-186	Sequence 186, App
44	294.5	21.4	3300	15 US-10-037-270-456	Sequence 456, App
45	294.5	21.4	3300	17 US-10-117-722-456	Sequence 456, App

ALIGNMENTS

RESULT 1
US-09-778-963A-1
Sequence 1, Application US/09778963A
Patent No. US2002011572A1
GENERAL INFORMATION:
APPLICANT: NIELAM, Beena et al
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS, THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
FILE REFERENCE: CL001112
CURRENT APPLICATION NUMBER: US/09/778,963A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-778-963A-1

Alignment Scores:

Pred. No.:	3,12e-168	Length:	3082
Score:	1377.00	Matches:	266
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

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QY	1	MetMetLyThrLeuSerSerGlyAanCyThrLeuSerValProAlaLysAsnSerTyr	20
DB	211	ATGATGAAGAAGCTTTGTCACGGCGGAACCTGACAGCTCAAGTGTCCCGCCAAAGCTATAC	270
QY	21	ArgMetValIleuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu	40
DB	271	CGCATGTGTGTCTGTGGTGTCTGTGGGTGGCAAGACCTCATGTGTCTGTCTCTC	330
QY	41	AanGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr	60
DB	331	AATGCGCGCTTGAGAGACAGTACACACCCACACGAGCTTCCACCGTAAGTATAC	390
QY	61	AanIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe	80
DB	391	AACATCCCGCGGACATGTACCATCTCGACATCTGTGATCCTGTGGCAACCACTTC	450
QY	81	ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu	100
DB	451	CCCCGATCGGACAGCTGTCCATCTTCACAGGAGTGTCTTCATCTGTGTTCAGCTG	510
QY	101	AspAanArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluValLys	120
DB	511	GATAACCGGAGTCTCTGTGATGAGGTCAAGCGCTTCAGAAAGATCTGTGAGTCAAG	570
QY	121	SerCyLeuLysAsnLysThrLysGluAlaIleGluLeuProMetValIleCySerGlyAsn	140
DB	571	TCTGTCTGAAAGAACAAAGACCAAGAGCGCGAGCTGCCCATGTGATCTGTGGCAAC	630
QY	141	LysAsnAspHisGlyGluLeuCyArgGluValProThrThrGluAlaGluLeuValLys	160
DB	631	AAGAAGCAACACCGGAGCTGTGCGCCAGGTGCCACACCGAGCGGAGCTGTGTGTG	690
QY	161	SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp	180
DB	691	TGGGCGGACGAGACTCGCTTCACTTCAGAGGTGTGGCCAAAGAAACACCAACGTGCAC	750
QY	181	GluMetPheTyrValIleuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu	200
DB	751	GAGATGTTCTACGTGCTCTTCAGCATGAGCCAAAGCTGCACACGAGATGAGCCCCGCTG	810
QY	201	HisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCySerMetArg	220
DB	811	CATGCAAGATCTCGGTGACAGTACGTGACGCTTCACCCCAAGCCCTTCTCATATGCC	870
QY	221	ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal	240
DB	871	CGGCTCAAGAGATGAGCGCTTGTGATGATGTCTCGCCCTTCCGCCCGCCCAAGGTG	930
QY	241	AsnSerAspLeuLysTyrIleLysAlaLysValLeuArgGluGlnIleAlaArgGluLys	260
DB	931	AACGATACCTCAAGTACATCAAGGCCAAAGGTCTTCGGGAAAGCCAGGCCCTGTGAAG	990
QY	261	AspLysCySerThrIleGln	266
DB	991	GACAAAGTGCACCATCCAG	1008

RESULT 2

US-10-804-491-40
; Sequence 40, Application US/10804491
; Publication No. US20040180375A1
; GENERAL INFORMATION:
; APPLICANT: Ciemoweki, Mary
; APPLICANT: Duzic, Emir

;; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
;; FILE REFERENCE: 60388-A-PCT-US
;; CURRENT APPLICATION NUMBER: US/10/804,491
;; CURRENT FILING DATE: 2004-03-19
;; PRIORITY APPLICATION NUMBER: US/09/709,103
;; PRIORITY FILING DATE: 2000-11-08
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 40
;; LENGTH: 837
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(834)
;; OTHER INFORMATION:
US-10-804-491-40

Alignment Scores:

Pred. No.:	1.8e-168	Length:	837
Score:	1372.00	Matches:	265
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Best Local Similarity:	99.62%	Mismatches:	1
Query Match:	99.64%	Indels:	0
DB:	18	Gaps:	0

US-09-778-963B-2 (1-266) x US-10-804-491-40 (1-837)

QY	1	MetMetLyThrLeuSerSerGlyAanCyThrLeuSerValProAlaLysAsnSerTyr	20
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QY	21	ArgMetValIleuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu	40
DB	97	CGCATGTGTGTCTGTGGTGTCTGTGGGTGGCAAGACCTCATGTGTCTGTCTCTC	156
QY	41	AanGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr	60
DB	157	AATGCGCGCTTGAGAGACAGTACACACCCACACGAGCTTCCACCGTAAGTATAC	216
QY	61	AanIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe	80
DB	217	AACATCCCGGAGACATGTACCATCTCGACATCTGTGATCCTGTGCAACCACTTC	276
QY	81	ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu	100
DB	277	CCCCGATCGGACAGCTGTCCATCTTCACAGGAGTGTCTTCATCTGTGTTCAGCTG	336
QY	101	AspAanArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluValLys	120
DB	337	GATTAACCGGAGTCTCTGTGATGAGGTCAAGCGCTTCAGAAAGATCTGTGAGTCAAG	396
QY	121	SerCyLeuLysAsnLysThrLysGluAlaIleGluLeuProMetValIleCySerGlyAsn	140
DB	397	TCTGTCTGAAAGAACAAAGACCAAGAGCGCGGAGTGCCCAAGTCACTGTGTGCAAC	456
QY	141	LysAsnAspHisGlyGluLeuCyArgGluValProThrThrGluAlaGluLeuValLys	160
DB	457	AAGAAGCAACACCGGAGCTGTGCGCCAGGTGCCACACCGAGCGGAGCTGTGTGTG	516
QY	161	SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp	180
DB	517	TGGGCGGACGAGACTGCGCTTCAAGTGTGTGAGGTGTGCGCCAAAGAAACACCAAGTGCAC	576
QY	181	GluMetPheTyrValIleuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu	200
DB	577	GAGATGTTCTACGTGCTCTTCAGCATGAGCCAAAGTGCACACGAGATGAGCCCCGCTG	636
QY	201	HisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCySerMetArg	220
DB	637	CATGCAAGATCTCGGTGACAGTACGTGAGCGCTTCCACCCCAAGCCCTTCTCATATGCC	696
QY	221	ArgValLysGluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal	240

DB 697 CGCGTCAAGAGATGAGCGCCATGCGCTGCGCCCTTGCAGCCGCGCCGAGCCCTC 756
QY 241 AanserApleuYrYrIleYyAlaYValleuArgIugIyGlnAlaArgIuArg 260
DB 757 AACAGTGAACCTCAAGTATCATCAAGGCCAAGGCTCTTGGGAAGGCCAGGCCGTGAGAG 816
QY 261 AsplysCythrIleGln 266
DB 817 GACAAAGTCAACCATCCAG 834
RESULT 3
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; Sequence 174, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-715-174
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Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
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QY 1 MetMetLyThrLeuSerSerGIYAAnCythrLeuSerValProAlaYAsnSerTyr 20
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QY 21 ArgMetValValleuGIYAlaSerArgValGIYLySerSerIleValSerArgPheLeu 40
DB 97 CGCATGGTGTGTGCTGGTGCCTCTCGGTGGGCAAGACTCATGTGTCTCGTCTCTC 156
QY 41 AsnGIYArgPheGIYAspGlnTyrThrProThrIleGIYAspPheHisArgLyValTyr 60
DB 157 AATGGCCGCTTGAAGACAGTACACACCAACCACTGAGACTTCCACCGTAGATTATAC 216
QY 61 AsnIleArgGIYAspMetTyrGlnLeuAspIleLeuAspThrSerGIYAsnHisProPhe 80
DB 217 AACATCCGCGCGACATATACAGCTCGACATCTCGATACCTCTGGCAACCAACCCCTTC 276
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGIYAspValPheIleLeuValPheSerLeu 100
DB 277 CCGCGCATGCCCAAGCTGTCCATCTCAAGGGAGATGCTTCATCTGTGTTCAGCTG 336
QY 101 AspAsnArgGIYSerPheAspGIYValLyArgLeuGlnLyGlnIleLeuGlnValLy 120
DB 337 GATAACCGGAGTCTCTGATGAGGTCAAGCGCTTCAAGAGCAGATCTGAGGTCAAG 396
QY 121 SerCyAspLeuLyAsnLyThrLyArgIuAlaIleGlnLeuProMetValIleCyArgGIYAsn 140

DB 397 TCCTGCTGAAGAACCAAGCAAGAGCGGAGCTGCCATGATGTATCTGTGCGAAC 456
QY 141 LyAsnAspHisArgIYLeuCyArgGlnValProThrThrGlnAlaGlnLeuVal 160
DB 457 AAGAACCAACCAAGCGAGCTGTGTGCGCAGGTGCCACACCGAGGCCGAGCTGTGTG 516
QY 161 SerGIYAspGIYAsnSerAlaTyrPheGIYValSerAlaYValYAsnThrAsnValAsp 180
DB 517 TCGGGCAACAGAACTGCGCTTACTTGAAGTGTGCGCCAGAAAGAACCAACCATGTGAC 576
QY 181 GluMetPheTyrValLeuPheSerMetAlaYLeuProHisGlnMetSerProAlaLeu 200
DB 577 GAGATGTCTTCAAGTGTCTTCAAGTGTCCAGAGTGCACACGAGATGAGCCCGGCTG 636
QY 201 HisArgLyValSerValGlnTyrGIYAspAlaPheHisProArgProPheCyMetArg 220
DB 637 CATGCAAGATCTTCCGTCAGTACAGTGAAGCGCTTCCACCCAGCCCTTGTGATCGC 696
QY 221 ArgValLyGIYMetAspAlaTyrGIYMetValSerProPheAlaArgProSerVal 240
DB 697 CGCGTCAAGAGATGAGCGCTTATGCAATGTCTCGCCCTTCCGCCCGCCGAGAGCTC 756
QY 241 AanserApleuYrYrIleYyAlaYValleuArgIugIyGlnAlaArgIuArg 260
DB 757 AACAGTGAACCTCAAGTATCATCAAGGCCAAGGCTCTTGGGAAGGCCAGGCCGTGAGAG 816
QY 261 AsplysCythrIleGln 266
DB 817 GACAAAGTCAACCATCCAG 834
RESULT 4
US-10-185-035-4
; Sequence 4, Application US/10185035
; Publication No. US20040005706A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Doobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DEXRAS1 EXPRESSION
; FILE REFERENCE: RTS-0377
; CURRENT APPLICATION NUMBER: US/10/185,035
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 4
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(837)
US-10-185-035-4
Alignment Scores:
Pred. No.: 1,236-167 Length: 2832
Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
Gaps: 0
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QY 1 MetMetLyThrLeuSerSerGIYAAnCythrLeuSerValProAlaYAsnSerTyr 20
DB 37 ATGATGAAGACTTGTTCACGCGGGAACCTGACGCTCAGTGTGCGCCGCAAAACTCATAC 96
QY 21 ArgMetValValleuGIYAlaSerArgValGIYLySerSerIleValSerArgPheLeu 40
DB 97 CGCATGGTGTGTGCTGGTGCCTCTCGGTGGGCAAGACTCATGTGTCTCGTCTCTC 156
QY 41 AsnGIYArgPheGIYAspGlnTyrThrProThrIleGIYAspPheHisArgLyValTyr 60
DB 157 AATGGCCGCTTGAAGACAGTACACACCAACCACTGAGACTTCCACCGTAGATTATAC 216


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QY 61 AenlleargGlyAspMetTyrGlnLeuaspilleleuaspThrSerGlyAsnHisProphe 80
DB 217 AACATCCGGCGGACATGTACAGCTCGACATCTCGATACCTCTGGCAACCCCTTC 276
QY 81 ProAlaMetArgArgLeuSerIleLeuThrgIyaAPValPheIleLeuValPheSerLeu 100
DB 277 CCCGCCATCGCAGAGCTGTCATCTCTCACAGGGAGATGCTTCATCTCTGTTCAGCCTG 336
QY 101 AspaAnaArgIuSerPheaspGluValIySaArgLeuGlnIySeriIleLeuGluValIys 120
DB 337 GATTAACCGGAGTCTTCGATGAGGTCAAGCCCTTCAGAGCATCTCTGAGGTCAAG 396
QY 121 SerCyLeuIySaAsnIySerThrySgluaIaIaGluLeuPrometValIleCySglYAsn 140
DB 397 TCCTGCTCGAAGAACAAACAGAGAGCGCGGAGCTGCCATGTCATCTGTGGCAAC 456
QY 141 LySaAnaSPHieGlyGluLeuCySaArgGlnValProThrThrgIuaIaGluLeuVal 160
DB 457 AAGAACGACACGCGGAGCTGTGCGCGAGGCCACACGAGGCCGAGCTGTGCTG 516
QY 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaIySeriIySaAsnThraSnaValAsp 180
DB 517 TCGGCGACGAGAACCTGCGCTACTTCAGAGGTGTCGCGCAAGAACACCAACGAGTGAC 576
QY 181 GluMetPheTyrValLeuPheSerMetAlaIySeriProHisGluMetSerProAlaLeu 200
DB 577 GAGATGTTCTACGTCTCTTCAGCATGCGCAAGCTGCCACACGAGATGAGCCCTG 636
QY 201 HisArgIySeriIeSerValGlnTyrGlyAspAlaPheHisProArgProPheCyMetArg 220
DB 637 CATGCGAAGATCTCGGTGACGTACGTGACCGCTTCACCCGAGCCCTTCGATCGC 696
QY 221 ArgValIySgluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal 240
DB 697 CGCGTCAGAGAGATGAGCGCTTATGCAATGATCTCGCCCTTCGCGCGCGCCAGGCTC 756
QY 241 AsnSerAspLeuIyTyrIleIySaAlaIySeriValLeuArgGluGlnIaIaArgGluArg 260
DB 757 AACAGTAGCTCAAGTACATCAAGGCCAAGSTCTTCGGGAGAGGCCAGGCCCGTGAAGAG 816
QY 261 AspIySeriThryIleGln 266
DB 817 GACAAGTGCACCATTCAG 834

```

RESULT 5

```

US-10-474-794-174
; Sequence 174, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-474-794-174

```

Alignment Scores:

```

Pred. No.: 1,236-167
Score: 1372.00
Percent Similarity: 99.62%

```

```

Length: 2832
Matches: 265
Conservative: 0

```

```

Best Local Similarity: 99.62%
Query Match: 99.64%
DB: 18
Gaps: 0

```

```

US-09-778-963b-2 (1-266) x US-10-474-794-174 (1-2832)

```

```

QY 1 MetMetIySeriThryLeuSerSerGlyIyAsnCySeriThryLeuSerValProAlaIySaAsnSerTyr 20
DB 37 ATGATAGACCTTTGTCCACCGGAACTGACAGCTTCAGATGTGCTCCGCAAAACTCATAC 96
QY 21 ArgMetValIaIeGluGlyIaSerArgValIySeriIySeriIyValSerArgPheLeu 40
DB 97 CGATGTGTGTGCTGTGTGCTCTCTCGGTGGGCAAGCTTCATGTGTCTGTCTCTTC 156
QY 41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgIySeriValTyr 60
DB 157 AATGCCGCTTTGAGAGACCATGACACACCATCATGAGACCTTCACCGTAAAGGTATAC 216
QY 61 AenlleargGlyAspMetTyrGlnLeuaspilleleuaspThrSerGlyAsnHisProphe 80
DB 217 AACATCCGGCGGACATGTACAGCTCGACATCTCGATACCTCTGGCAACCCCTTC 276
QY 81 ProAlaMetArgArgLeuSerIleLeuThrgIyaAPValPheIleLeuValPheSerLeu 100
DB 277 CCCGCCATCGCAGAGCTGTCATCTCTCACAGGGAGATGCTTCATCTCTGTTCAGCCTG 336
QY 101 AspaAnaArgIuSerPheaspGluValIySaArgLeuGlnIySeriIleLeuGluValIys 120
DB 337 GATTAACCGGAGTCTTCGATGAGGTCAAGCCCTTCAGAGCATCTCTGAGGTCAAG 396
QY 121 SerCyLeuIySaAsnIySerThrySgluaIaIaGluLeuPrometValIleCySglYAsn 140
DB 397 TCCTGCTCGAAGAACAAACAGAGAGCGCGGAGCTGCCATGTCATCTGTGGCAAC 456
QY 141 LySaAnaSPHieGlyGluLeuCySaArgGlnValProThrThrgIuaIaGluLeuVal 160
DB 457 AAGAACGACACGCGGAGCTGTGCGCGAGGCCACACGAGGCCGAGCTGTGCTG 516
QY 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaIySeriIySaAsnThraSnaValAsp 180
DB 517 TCGGCGACGAGAACCTGCGCTACTTCAGAGGTGTCGCGCAAGAACACCAACGAGTGAC 576
QY 181 GluMetPheTyrValLeuPheSerMetAlaIySeriProHisGluMetSerProAlaLeu 200
DB 577 GAGATGTTCTACGTCTCTTCAGCATGCGCAAGCTGCCACACGAGATGAGCCCGCTG 636
QY 201 HisArgIySeriIeSerValGlnTyrGlyAspAlaPheHisProArgProPheCyMetArg 220
DB 637 CATCGCAAGATCTCGTCAAGTACGTGACGCTTCACCCGAGCCCTTCGATGAGC 696
QY 221 ArgValIySgluMetAspAlaTyrGlyMetValSerProPheAlaArgArgProSerVal 240
DB 697 CGCGTCAGAGAGATGAGCGCTTATGCAATGATCTCGCCCTTCGCGCGCGCCAGGCTC 756
QY 241 AsnSerAspLeuIyTyrIleIySaAlaIySeriValLeuArgGluGlnIaIaArgGluArg 260
DB 757 AACAGTAGCTCAAGTACATCAAGGCCAAGSTCTTCGGGAGAGGCCAGGCCCGTGAAGAG 816
QY 261 AspIySeriThryIleGln 266
DB 817 GACAAGTGCACCATTCAG 834

```

RESULT 6

```

US-09-918-715-197
; Sequence 197, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715

```

CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 197
LENGTH: 2973
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-715-197

Alignment Scores:
Pred. No.: 1,32e-167 Length: 2973
Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
Gaps: 0

US-09-778-963b-2 (1-266) x US-09-918-715-197 (1-2973)

Qy 1 MetMetLyThrLeuSerSerGlyAaenCyThrLeuSerValProAlaLysAaenSerTyr 20
Db 208 ATGATGAAGACTTGTTCACAGGGGAACTGACGCTCACTGTGCGCCCAAAACTCATAC 267

Qy 21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db 268 CGCATGTGTGTCTGGGTCTCTCGGTGGGCAAGACTCATCTGTCTCGCTTCTC 327

Qy 41 AaenGlyArgPheGluAaenGlyTyrThrProThrIleGluAaenPheHisArgLysValTyr 60
Db 328 AATGGCGGCTTTGAGGACCACTACACCACTCGAGACTTCACCGTAAGGTATAC 387

Qy 61 AaenIleArgGlyAaenMetTyrGlnLeuAaenIleLeuAaenThrSerGlyAaenHisProPhe 80
Db 388 AACATCGCGGCGCATGTATACAGCTCGACATCTGTGATACCTCTGGCAACCCCTTC 447

Qy 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAaenValPheIleLeuValPheSerLeu 100
Db 448 CCGCCCATCGGCAAGCTCTCATCTCTCAAGGGATGTCTTCACTCTGTTCAAGCTG 507

Qy 101 AaenAaenArgGluSerPheAaenGluValLysArgLeuGlnLysGlnIleLeuGluValLys 120
Db 508 GATAACGGGAGTCTCTTGATGAGGTCAAGCGCTTCAGAAAGCATCTCGAGGTCAAG 567

Qy 121 SerCyLeuLeuLysAaenLysThrLysGlnAaenLysLeuAaenProMetValIleCyGlyAaen 140
Db 568 TCCTGCGCTTGAAGAACAAAGCAAGAGCGGCGGAGCTGCCATGTCTGTGGCAAC 627

Qy 141 LysAaenAaenHisGlyGluLeuCyAaenGlnValProThrThrGlnAaenLysLeuVal 160
Db 628 AAGAACGACACCGGAGACTGTGCGGAGGTGCCACACCAAGGCCGAGCTCTGCTG 687

Qy 161 SerGlyAaenGluAaenSerAlaTyrPheGluValSerAlaLysLysAaenThrAaenValAaen 180
Db 688 TCGGCGGACGAGAACTGCGCTTCACTGAGGTGTGCGCAAGAAACCAAGAGTGAAC 747

Qy 181 GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
Db 748 GAGATGTCTTACGAGCTCTTCAAGATGCGCAAGCTGCCACAGATGAAGCCCGCTG 807

Qy 201 HisArgLysIleSerValGlnTyrGlyAaenAlaPheHisProAaenProPheCyMetArg 220
Db 808 CATGCGAAGATCTCGGTCAAGTACGGTACCGCTTCCACCCAGGCCCTTGTGATGGC 867

Qy 221 ArgValLysGluMetAaenAlaTyrGlyMetValSerProPheAlaArgArgProSerVal 240
Db 868 CGGCTCAAGAGATGAGCGCTTATGAGATGTCTGCGCTTCCGCGCGCGCCAGCGTC 927

Qy 241 AaenSerAaenLysTyrIleLysAlaLysValLeuArgGluGlnAaenArgGluArg 260
Db 928 AACAGTACCTTCAAGTACATCAAGGCCAAGGTCTTCTGGAAAGGCCCGCTGAGAG 987

Qy 261 AaenLysCyThrIleGln 266
Db 988 GACAGTGCACCATCCAG 1005

RESULT 7
US-10-474-794-197
Sequence 197, Application US/10474794
Publication No. US20040213793A1
GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107,00179
CURRENT APPLICATION NUMBER: US/10/474,794
PRIOR FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 197
LENGTH: 2973
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-197

Alignment Scores:
Pred. No.: 1,32e-167 Length: 2973
Score: 1372.00 Matches: 265
Percent Similarity: 99.62% Conservative: 0
Best Local Similarity: 99.62% Mismatches: 1
Query Match: 99.64% Indels: 0
Gaps: 0

US-09-778-963b-2 (1-266) x US-10-474-794-197 (1-2973)

Qy 1 MetMetLyThrLeuSerSerGlyAaenCyThrLeuSerValProAlaLysAaenSerTyr 20
Db 208 ATGATGAAGACTTGTTCACAGGGGAACTGACGCTCACTGTGCGCCCAAAACTCATAC 267

Qy 21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
Db 268 CGCATGTGTGTCTGGGTCTCTCGGTGGGCAAGACTCATCTGTCTCGCTTCTC 327

Qy 41 AaenGlyArgPheGluAaenGlyTyrThrProThrIleGluAaenPheHisArgLysValTyr 60
Db 328 AATGGCGGCTTTGAGGACCACTACACCACTCGAGACTTCACCGTAAGGTATAC 387

Qy 61 AaenIleArgGlyAaenMetTyrGlnLeuAaenIleLeuAaenThrSerGlyAaenHisProPhe 80
Db 388 AACATCGCGGCGCATGTATACAGCTCGACATCTGTGATACCTCTGGCAACCCCTTC 447

Qy 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAaenValPheIleLeuValPheSerLeu 100
Db 448 CCGCCCATCGGCAAGCTCTCATCTCTCAAGGGATGTCTTCACTCTGTTCAAGCTG 507

Qy 101 AaenAaenArgGluSerPheAaenGluValLysArgLeuGlnLysGlnIleLeuGluValLys 120
Db 508 GATAACGGGAGTCTCTTGATGAGGTCAAGCGCTTCAGAAAGCATCTCGAGGTCAAG 567

Qy 121 SerCyLeuLeuLysAaenLysThrLysGlnAaenLysLeuAaenProMetValIleCyGlyAaen 140
Db 568 TCCTGCGCTTGAAGAACAAAGCAAGAGCGGCGGAGCTGCCATGTCTGTGGCAAC 627

Qy 141 LysAaenAaenHisGlyGluLeuCyAaenGlnValProThrThrGlnAaenLysLeuVal 160

Db 628 AAGAACGACGAGCGAGCTGTCGCGCCAGGTCGCCACACCGAGCCGAGCTGCTGTCG 687
 QY 161 SERGIYASPGIUAASerIATyrPheGIUValSerIAlaLYsAlaThrAsnValAsp 180
 Db 688 TCGGGGAGAGAACTGCGCCCTTACTTCGAGGTGTGGCGCCAGAGAAACACCAACGTGAC 747
 QY 181 GIUmetPheTYrValIleuPheSerMetAlaLYsLeuProHISGIUmetSerProAlaIleu 200
 Db 748 GAGATGTTCTTACGTCTCTTCAGCATGCGCCAGCTGCCACACGAGATGAGCCCGCTG 807
 QY 201 HISArgLYsIleSerValGIUInTYrGIYAspAlaPheHISProArgProPheCYsMetArg 220
 Db 808 CATCCCAAGATCTCCGTGAGTACGCTGACGCTTCCACCCAGGCCCTTCGTGATGCGC 867
 QY 221 ArgValLYsGIUmetAspAlaTYrGIYMetValSerProPheAlaArgArgProSerVal 240
 Db 868 CGCGTCAGAGAGATGAGCGCTATGCAATGCTGCGCTTCGCGCGCGCCGACGCTC 927
 QY 241 AsnSerAspLeuLYsTYrIleLYsAlaLYsValIleuArgGIUInTYrAlaArgGIUArg 260
 Db 928 AACAGTGAACCTCAAGTATCATCAAGGCCAAGGTCCTTCGGGAAGGCCAGGCCCGGTGAGAG 987
 QY 261 AspLYsCYsThrIleGIU 266
 Db 988 GACAGTGCACCATTCAG 1005

RESULT 8

US-10-723-860-5134
 ; Sequence 5134, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Nataasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnick, Albert
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
 ; FILE REFERENCE: 05882, 0193, NEUS01
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 5134
 ; LENGTH: 3058
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-723-860-5134

Alignment Scores:

Pred. No.: 1,38e-167 Length: 3058
 Score: 1372.00 Matches: 265
 Percent Similarity: 99.62% Conservative: 0
 Best Local Similarity: 99.62% Mismatches: 1
 Query Match: 99.64% Indels: 0
 DB: 18 Gaps: 0

US-09-778-963b-2 (1-266) x US-10-723-860-5134 (1-3058)

QY 1 MetMetLYsThrIleuSerSerGIYAsnCYsThrIleuSerValProAlaLYsAsnSerTYr 20
 Db 217 ATGATGAAGACTTGTTCAGCGGGAGACTGCACGCTCAGTGTGCCCGCAAAAACCTATAC 276
 QY 21 ArgMetValValIleuGIYAlaSerArgValGIYLYsSerSerIleValSerArgPheLeu 40
 Db 277 CGCATGTGTGTGGTGTGCTCTCGGGTGGCAAGCTTCATCTGTCTCGCTTCCTC 336
 QY 41 AsnGIYArgPheGIUAspGIUInTYrThrProThrIleGIUAspPheHISArgLYsValTYr 60
 Db 337 AATGGCGCGCTTGAAGACAGTACACACCAACCATCGAGACTTCACCGTAAGGTATAC 396
 QY 61 AsnIleArgGIYAspMetTYrGIUInleuAspIleLeuAspThrSerGIYAsnHISProPhe 80

Db 397 AACATCCGCGGCGAGATGTACCAAGCTTCGACATCTGAGATACCTCTGGCAACCAACCCCTTC 456
 QY 81 ProAlaMetArgArgIleuSerIleLeuThrGIYAspValPheIleLeuValPheSerLeu 100
 Db 457 CCGGCATGCGAGAGGCTGTCCATCTCCACAGGGAGATCTTCACTCTGCTGTTCACGCTG 516
 QY 101 AspAsnArgGIUSerPheAspGIUValLYsArgLeuGIUInLYsGIUInLYsValLYs 120
 Db 517 GATTAACGGGAGTCTCTCGATGAGTCAAGCGCTTCAGAGAGATCTCTGAGGTCAG 576
 QY 121 SerCYsLeuLYsAsnLYsThrLYsGIUAlaIAGIleuProMetValIleCYsGIYAsn 140
 Db 577 TCTGCTGTAAAGAACAGACAGAGAGGCGGAGACTCCCATGTGTCTGTGCAAC 636
 QY 141 LYsAsnAspHISGIYGIUleuCYsArgGIUValProThrThrGIUAlaGIUleuLeuVal 160
 Db 637 AAGAACGACACCGGAGCTGTGCGCCAGGTGCCACACCGAGGCCGAGCTGTGCTG 696
 QY 161 SERGIYASPGIUAASerIATyrPheGIUValSerIAlaLYsAlaThrAsnValAsp 180
 Db 697 TCGGGGAGAGAACTGCGCTTACTTCGAGGTGTGGCCAGAGAACCAACGTCGAC 756
 QY 181 GIUmetPheTYrValIleuPheSerMetAlaLYsLeuProHISGIUmetSerProAlaIleu 200
 Db 757 GAGATGTTCTTACGTCTCTTCAGCATGCGCCAGCTGCCACAGAGATGAGCCCGCTG 816
 QY 201 HISArgLYsIleSerValGIUInTYrGIYAspAlaPheHISProArgProPheCYsMetArg 220
 Db 817 CATCGCAAGATCTCCGTGAGTACGCTGACGCTTCCACCCAGGCCCTTCGTGATGCGC 876
 QY 221 ArgValLYsGIUmetAspAlaTYrGIYMetValSerProPheAlaArgArgProSerVal 240
 Db 877 CGCGTCAGAGAGATGAGCGCTATGCAATGCTGCGCTTCGCGCGCGCCGACGCTC 936
 QY 241 AsnSerAspLeuLYsTYrIleLYsAlaLYsValIleuArgGIUInTYrAlaArgGIUArg 260
 Db 937 AACAGTGAACCTCAAGTATCATCAAGGCCAAGGTCCTTCGGGAAGGCCAGGCCCGGTGAGAG 996
 QY 261 AspLYsCYsThrIleGIU 266
 Db 997 GACAGTGCACCATTCAG 1014

RESULT 9

US-09-918-715-292
 ; Sequence 292, Application US/09918715
 ; Publication No. US20030017157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brad St. Croix
 ; APPLICANT: Bert Vogelstein
 ; APPLICANT: Kenneth Kinzler
 ; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
 ; FILE REFERENCE: 1107, 00134
 ; CURRENT APPLICATION NUMBER: US/09/918, 715
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/222,599
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: 60/224,360
 ; PRIOR FILING DATE: 2000-08-11
 ; PRIOR APPLICATION NUMBER: 60/282,850
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: PaetSeq for Windows Version 3.0
 ; SEQ ID NO 292
 ; LENGTH: 3020
 ; TYPE: DNA
 ; ORGANISM: Mouse
 US-09-918-715-292

Alignment Scores:

Pred. No.: 1.02e-158 Length: 3020
 Score: 1304.00 Matches: 252
 Percent Similarity: 96.24% Conservative: 4
 Best Local Similarity: 94.74% Mismatches: 10

Query Match: 94.70% Indels: 0
DB: 10 Gaps: 0

US-09-778-963B-2 (1-266) x US-09-918-715-292 (1-3020)

```
QY 1 MetMetlyThrLeuSerSerGlyAsnCyThrLeuSerValProAlaIysAsnSerTyr 20
DB 376 ATGATGAAGACCTTGTCCAGTGGGAACGACACCTCAATGTGCTCGTAAAGCTCTAC 435
QY 21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
DB 436 CGCATGTGTGTGGTGGCTCTCCCGAGTGGGCAAGACTCATGTGTCTCCGCTTCTC 495
QY 41 AenGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
DB 496 AATGGCCGCTTGGAGACCAAGACGCGCCACTATTCAGAGACTTTCATCGCAAGGTATAC 555
QY 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB 556 AACATCCACGGGAGCATGTATACAGCTGGATATCCCTGGACACTCTCGGCAACCACTTC 615
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
DB 616 CCTGCCATGCGCGGCTCTCCATCTCTCAAGAGATGTCTTCATCTGTGTTCAGCTG 675
QY 101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluValLys 120
DB 676 GATAGCCGGAGTCTTGTATGAGGTCAAGCGCTCCGAAACAGATCTGAGGTCAAG 735
QY 121 SerCySLeuLysAsnLysThrLysGlnLysAlaGluLeuAspMetValIleCySGLYAsn 140
DB 736 TCCGTGCTGAAGATTAACCAAGAGGACAGACGCTGCCATGTGTATCTGTGGAAAC 795
QY 141 LysAsnAspHisGlyGlnLeuCyArgGlnValProThrThrGluAlaGluLeuVal 160
DB 796 AAGATGACACACAGTGAAGCTGTGCGCAGAGTCCCTGCATGAGAGCTGAGCTGTG 855
QY 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp 180
DB 856 TCTGTGTATGAACCTGCGCTATTTCCAGGTGTCAGGCAAGAAACATTAATGTGAAC 915
QY 181 GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
DB 916 GAGATGTTCTATGTGCTTTCAGCATGSCCAAGCTGCCATGATGAGCCCTGCACTG 975
QY 201 HisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCySmetArg 220
DB 976 CACCATAAAGATCTCGTGCAGTACGCGCATGCTTTTCACCCCGCGCTTCTGCATGCGT 1035
QY 221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheHisArgArgProSerVal 240
DB 1036 CGCATTAAGTGGCAGGTGCTTATGGCAATGATCTTCCCTTGGCCGCGCCAGTGTTC 1095
QY 241 AsnSerAspLeuLysTyrIleLysAlaLysValLeuArgGlnGlyAlaArgLysVal 260
DB 1096 AACGTGACCTCAAGTACATCAAGGCAAGGTCTTCAAGGAGGCGCCGAGAGAGG 1155
QY 261 AspLysCyThrIleGln 266
DB 1156 GACAAAGTGTACATCCAG 1173
```

RESULT 10

US-10-474-794-292
; Sequence 292, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Bred
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794

;; CURRENT FILING DATE: 2003-10-14
;; PRIOR APPLICATION NUMBER: 60/282,850
;; PRIOR FILING DATE: 2001-04-11
;; PRIOR APPLICATION NUMBER: 60/308,829
;; PRIOR FILING DATE: 2001-08-01
;; NUMBER OF SEQ ID NOS: 359
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 292
;; LENGTH: 3020
;; TYPE: DNA
;; ORGANISM: Mouse
US-10-474-794-292

Alignment Scores:

Pred. No.:	1,02e-158	Length:	3020
Score:	1304.00	Matches:	252
Percent Similarity:	96.24%	Conservative:	4
Best Local Similarity:	94.74%	Mismatches:	10
Query Match:	94.70%	Indels:	0
DB:	18	Gaps:	0

US-09-778-963B-2 (1-266) x US-10-474-794-292 (1-3020)

```
QY 1 MetMetlyThrLeuSerSerGlyAsnCyThrLeuSerValProAlaIysAsnSerTyr 20
DB 376 ATGATGAAGACCTTGTCCAGTGGGAACGACACCTCAATGTGCTCGTAAAGCTCTAC 435
QY 21 ArgMetValValLeuGlyAlaSerArgValGlyLysSerSerIleValSerArgPheLeu 40
DB 436 CGCATGTGTGTGGTGGCTCTCCCGAGTGGGCAAGACTCATGTGTCTCCGCTTCTC 495
QY 41 AenGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHisArgLysValTyr 60
DB 496 AATGGCCGCTTGGAGACCAAGACGCGCCACTATTCAGAGACTTTCATCGCAAGGTATAC 555
QY 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 80
DB 556 AACATCCACGGGAGCATGTATACAGCTGGATATCCCTGGACACTCTCGGCAACCACTTC 615
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
DB 616 CCTGCCATGCGCGGCTCTCCATCTCTCAAGAGATGTCTTCATCTGTGTTCAGCTG 675
QY 101 AspAsnArgGluSerPheAspGluValLysArgLeuGlnLysGlnIleLeuGluValLys 120
DB 676 GATAGCCGGAGTCTTGTATGAGGTCAAGCGCTCCGAAACAGATCTGAGGTCAAG 735
QY 121 SerCySLeuLysAsnLysThrLysGlnLysAlaGluLeuAspMetValIleCySGLYAsn 140
DB 736 TCCGTGCTGAAGATTAACCAAGAGGACAGACGCTGCCATGATGAGCCCTGCGGAAC 795
QY 141 LysAsnAspHisGlyGlnLeuCyArgGlnValProThrThrGluAlaGluLeuVal 160
DB 796 AAGATGACACACAGTGAAGCTGTGCGCAGAGTCCCTGCATGAGAGCTGAGCTGTG 855
QY 161 SerGlyAspGluAsnSerAlaTyrPheGluValSerAlaLysLysAsnThrAsnValAsp 180
DB 856 TCTGTGTATGAACCTGCGCTATTTCCAGGTGTCAGGCAAGAAACATTAATGTGAAC 915
QY 181 GluMetPheTyrValLeuPheSerMetAlaLysLeuProHisGluMetSerProAlaLeu 200
DB 916 GAGATGTTCTATGTGCTTTCAGCATGSCCAAGCTGCCATGATGAGCCCTGCACTG 975
QY 201 HisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCySmetArg 220
DB 976 CACCATAAAGATCTCGTGCAGTACGCGCATGCTTTTCAAGGAGGCGCCGAGAGAGG 1035
QY 221 ArgValLysGluMetAspAlaTyrGlyMetValSerProPheHisArgArgProSerVal 240
DB 1036 CGCATTAAGTGGCAGGTGCTTATGGCAATGATCTTCCCTTGGCCGCGCCAGTGTTC 1095
QY 241 AsnSerAspLeuLysTyrIleLysAlaLysValLeuArgGlnGlyAlaArgLysVal 260
```

Db 1096 AACAGTACCTCAAGTACATCAAGGCCAGGCTCTACGGGAGGCCAGGCCGAGAGAGG 1155
Qy 261 AApPvCyThrllegln 266
Db 1156 GACAAAGTATGATCCAG 1173

RESULT 11

US-09-778-963A-3
; Sequence 3, Application US/09778963A
; Patent No. US20020115172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; FILE REFERENCE: C1001112
; CURRENT APPLICATION NUMBER: US/09/778,963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-3

Alignment Scores:

Pred. No.:	1,566-106	Length:	11221
Score:	911.00	Matches:	176
Percent Similarity:	98.33%	Conservative:	1
Best Local Similarity:	97.78%	Mismatches:	3
Query Match:	66.16%	Indels:	0
DB:	9	Gaps:	0

US-09-778-963B-2 (1-266) x US-09-778-963A-3 (1-11221)

Qy 87 SerileuThrglyAspValPheileuValPheSerleuAspAsnArgLysSerPhe 106
Db 7681 TCTCTCCCTGAGGGAGGATGCTTCTCATCTGCTGTTACCTGATTAACCGGAGCTCTTC 7740
Qy 107 AspGluValLysArgLeuGlnLysGlnLysGlnLysSerCysLeuLysAsnLys 126
Db 7741 GATGAGTCAAGCGCTTCAAGACAGATCTGAGGCTCAAGCTCTGCAAGAACAG 7800
Qy 127 ThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyGlu 146
Db 7801 ACCAAGAGGCGGGGAGGCTGCCATGCTCATCTGTGGCAACAGAACGACGAGGAG 7860
Qy 147 LeuCyArgGlnValProThrThrgLysGluLeuValSerGlyAspGluAsnSer 166
Db 7861 CTGTGCGCGCCAGGTGCCACACCGAGGCGGCTGCTGTGCTGGCGGCGAGAACTGC 7920
Qy 167 AlaTyrrPheGluValSerAlaLysAsnThrAsnValAspGluMetPheTyrrValLeu 186
Db 7921 GCCACTTCGAGGTGTGCGCCAGAAAGAACACCAAGGAGCGAGTGTCTACGTGCTC 7980
Qy 187 PheSerMetAlaLysLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
Db 7981 TTCAGCATGGCCAGAGTGCACACAGATGAGCCCGCCCTGCATGCCAAGATCTCCGTG 8040
Qy 207 GlnTyrrLysAspAlaPheHisPProArgProPheCysMetArgValLysGluMetAsp 226
Db 8041 CAGTACGGTACCGCTTCCACCCAGGCGCTTGTGCGCGCGCGCTCAAGAGATGAGC 8100
Qy 227 AlaTyrrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrr 246
Db 8101 GCCATATGCGATGTGTGCTGCTGCTGCGCCGCGCCCAAGCTCAACGTGACCTCAAGTAC 8160
Qy 247 IleLysAlaLysValLeuArgGlnGlyGlnAlaArgGluArgAspLysCysThrllegln 266
Db 8161 ATCAAGGCCAAGGCTCTTGGGAAAGGCCAGGCCGCTGAGAGGAGCAAGTGCACATCCAG 8220

RESULT 12

US-10-185-035-11
; Sequence 11, Application US/10185035
; Publication No. US20040005706A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DEXRASI EXPRESSION
; FILE REFERENCE: RTS-0377
; CURRENT APPLICATION NUMBER: US/10/185,035
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 11
; LENGTH: 16000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-185-035-11

Alignment Scores:

Pred. No.:	2,736-106	Length:	16000
Score:	911.00	Matches:	176
Percent Similarity:	98.33%	Conservative:	1
Best Local Similarity:	97.78%	Mismatches:	3
Query Match:	66.16%	Indels:	0
DB:	17	Gaps:	0

US-09-778-963B-2 (1-266) x US-10-185-035-11 (1-16000)

Qy 87 SerileuThrglyAspValPheileuValPheSerleuAspAsnArgLysSerPhe 106
Db 11913 TCTCTCCCTGAGGGAGGATGCTTCTCATCTGCTGTTACCTGATTAACCGGAGCTCTTC 11972
Qy 107 AspGluValLysArgLeuGlnLysGlnLysGlnLysSerCysLeuLysAsnLys 126
Db 11973 GATGAGTCAAGCGCTTCAAGACAGATCTGAGGCTCAAGCTCTGCTGCAAGAACAG 12032
Qy 127 ThrLysGluAlaAlaGluLeuProMetValIleCysGlyAsnLysAsnAspHisGlyGlu 146
Db 12033 ACCAAGAGGCGGGGAGGCTGCCATGCTCATCTGTGGCAACAGAACGACGAGGAG 12092
Qy 147 LeuCyArgGlnValProThrThrgLysGluLeuValSerGlyAspGluAsnSer 166
Db 12093 CTGTGCGCGCCAGGTGCCACACCGAGGCGGCTGCTGTGCTGGCGGCGAGAACTGC 12152
Qy 167 AlaTyrrPheGluValSerAlaLysAsnThrAsnValAspGluMetPheTyrrValLeu 186
Db 12153 GCCACTTCGAGGTGTGCGCCAGAAAGAACACCAAGGAGCGAGTGTCTACGTGCTC 12212
Qy 187 PheSerMetAlaLysLeuProHisGluMetSerProAlaLeuHisArgLysIleSerVal 206
Db 12213 TTCAGCATGGCCAGAGTGCACACAGATGAGCCCGCCCTGCATGCCAAGATCTCCGTG 12272
Qy 207 GlnTyrrLysAspAlaPheHisPProArgProPheCysMetArgValLysGluMetAsp 226
Db 12273 CAGTACGGTACCGCTTCCACCCAGGCGCTTGTGCGCGCGCTCAAGAGATGAGC 12332
Qy 227 AlaTyrrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuLysTyrr 246
Db 12333 GCCATATGCGATGTGTGCTGCTGCTGCGCCGCGCCCAAGCTCAACGTGACCTCAAGTAC 12392
Qy 247 IleLysAlaLysValLeuArgGlnGlyGlnAlaArgGluArgAspLysCysThrllegln 266
Db 12393 ATCAAGGCCAAGGCTCTTGGGAAAGGCCAGGCCGCTGAGAGGAGCAAGTGCACATCCAG 12452

RESULT 13

US-10-723-860-458
; Sequence 458, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

```
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIORITY APPLICATION NUMBER: 60/429,739
PRIORITY FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 458
LENGTH: 114771
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-458

Alignment Scores:
Pred. No.: 6,09e-105 Length: 114771
Score: 911.00 Matches: 176
Percent Similarity: 98.33% Conservative: 1
Best Local Similarity: 97.78% Mismatches: 3
Query Match: 66.16% Indels: 0
Gaps: 0
DB: 18

US-09-778-963b-2 (1-266) x US-10-723-860-458 (1-114771)

QY 87 SerIleuThrgIyAapValPheIleuValPheSerIleuAapAanArgLysPhe 106
| | | | |
DB 57913 TCTCTCCCTCGAGGGGATGCTTCACTCTGTTCAAGCTGATTAACGGGAGTCTTC 57972
| | | | |
QY 107 AapGluValIyAaGleuGlnIySerGlyAapGluValIySerGlyAapGluValIy 126
| | | | |
DB 57973 GATGAGGTCAAGCCCTTCAGAACAGATCTGAGGATCAAGTCTGCTGAAACAAAG 58032
| | | | |
QY 127 ThrIleGluValIyAaGluPheMetValIleGlyAaGluValIyAaGluValIy 146
| | | | |
DB 58033 ACCAAGAGGGGGGAGGAGTGGCCATGATCTGTGCAACAAAGCAACAGCGGAG 58092
| | | | |
QY 147 LeuCyAaGlnValIyProThrThrgIyAaGluPheValIySerGlyAapGluValIy 166
| | | | |
DB 58093 CTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 58152
| | | | |
QY 167 AlaTyPheGluValIySerAlaIyValIyAaGluValIyAaGluValIyAaGlu 186
| | | | |
DB 58153 GCCCACTTCAGAGGTGTGGCCCAAGAAACCAAGTGAAGATGTTCTACGTGCTC 58212
| | | | |
QY 187 PheSerMetAlaIyValIyPheProThrThrgIyAaGluPheValIySerGlyAa 206
| | | | |
DB 58213 TTCAGCATGGCGCAAGCTGCAACAGATGAGCCCGCTGATCCCAAGATCTCGTG 58272
| | | | |
QY 207 GlnTyGlnIyAaPheIleuValIyPheProThrThrgIyAaGluPheValIySer 226
| | | | |
DB 58273 CAGTACGGTACGCTTCACCCAGGCGCTTCGATGCGCCCGCTCAAGAGATGAGC 58332
| | | | |
QY 227 AlaTyGlnIyMetValIySerProPheIleuValIyAaGluPheValIyAaGlu 246
| | | | |
DB 58333 GCGTATGAGCATGTCTGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 58392
| | | | |
QY 247 IleValIyAaValIyLeuArgGlnIyGlnIyAaGluValIyAaGluValIyAa 266
| | | | |
DB 58393 ATCAAGGCGCAAGTCTTCGGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 58452
| | | | |

RESULT 14
US-10-029-386-20951
Sequence 20951, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
```

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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20951
LENGTH: 696
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL022334.1 SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN HEP2 LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EST HUMAN HIT: B1754083.1, EVALUATE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P10301, EVALUATE 4.00e-10
OTHER INFORMATION: NT HIT: g116168170, EVALUATE 0.00e+00
US-10-029-386-20951

Alignment Scores:
Pred. No.: 2.91e-107 Length: 696
Score: 902.00 Matches: 174
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 1
Query Match: 65.50% Indels: 0
Gaps: 0
DB: 16

US-09-778-963b-2 (1-266) x US-10-029-386-20951 (1-696)

QY 92 AapValPheIleuValPheSerIleuAapAanArgLysPheAapGluValIyAa 111
| | | | |
DB 3 GATGTCTTCACTCTGTTGATGCTTCACTGATTAACGGGAGTCTTCATGAGGATCAAGCC 62
| | | | |
QY 112 LeuGlnIySerGlnIyAaGluValIySerGlyAaGluValIyAaGluValIyAa 131
| | | | |
DB 63 CTTCAGAGGAGGAGTCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 122
| | | | |
QY 132 GlnIyPhePheValIyIleGlyAaGluValIyAaGluValIyAaGluValIyAa 151
| | | | |
DB 123 GACCTGCCCATGTGATCTGTGCAACAAAGCAACAGCGAGCTGCGCCGAGGTG 182
| | | | |
QY 152 ProThrThrgIyAaGluPheValIySerGlyAaGluValIyAaGluValIyAa 171
| | | | |
DB 183 CCACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
| | | | |
QY 172 SerAlaIyValIyAaGluValIyAaGluValIyAaGluValIyAaGluValIy 191
| | | | |
DB 243 TCGGCGCAAGAAACCAACAGTGAAGATGTTCTACGCTCTTCAGCAAGCGCAAG 302
| | | | |
QY 192 LeuProIleGlnIySerProAlaIyValIyAaGluValIyAaGluValIyAa 211
| | | | |
DB 303 CTGCCACAGAGATGAGCCCGCTGATCGCAAGATCTCGTCAAGTGAAGCGCC 362
| | | | |
QY 212 PheIleuProArgProPheCyMetAlaGluValIyGlnIyMetAlaIyValIy 231
| | | | |
DB 363 TTCACCCCGAGGCTTCGATGAGCGCGCGCTCAAGAGATGAGCGCGCTATGCGATGTC 422
| | | | |
QY 232 SerProPheIleuValIyAaGluPheValIyAaGluPheValIyAaGluPhe 251
| | | | |
DB 423 TCGCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 482
| | | | |
QY 252 LeuArgGlnIyGlnIyAaGluValIyAaGluValIyAaGluValIyAaGlu 266
| | | | |
DB 483 CTTCGGGAGGCGGAGGCGCGCTGAGAGGAGCAAGTGAAGTCAAGTCAAGTCAAG 527
| | | | |

RESULT 15
US-10-804-491-1
Sequence 1, Application US/10804491
Publication No. US20040180375A1
GENERAL INFORMATION:
APPLICANT: Ciernowski, Mary
APPLICANT: Duzic, Emir
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
FILE REFERENCE: 60388-A-PCR-US
CURRENT APPLICATION NUMBER: US/10/804,491
CURRENT FILING DATE: 2004-03-19
PRIORITY APPLICATION NUMBER: US/09/709,103
```

PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 846
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(843)
OTHER INFORMATION:
US-10-804-491-1

Alignment Scores:
Pred. No.: 3,97e-104 Length: 846
Score: 879.00 Matches: 172
Percent Similarity: 77.70% Conservative: 44
Best Local Similarity: 61.87% Mismatches: 46
Query Match: 63.83% Indels: 16
DB: 18 Gaps: 4

US-09-778-963b-2 (1-266) x US-10-804-491-1 (1-846)

```
QY 1 MetWetlysrThrLeuSerSerGlyAsnCystrHrLeuSerValProAlaIysAsnSerTyr 20
Db 16 ATGATCAAGAGATGTGCGCGAGACTCGAGCTGAGTATCCGGCCAGAACTGCTAT 75
QY 21 ArgMetValValLeuGlyAlaSerArgValGlyIysSerSerIleValSerArgPheLeu 40
Db 76 CGCATGGTCATCCGCTCGCTCCAGGTGGCAAGCGGCATCGTGTGCGGCTTCTC 135
QY 41 AsnGlyArgPheGluAspGlnTyrThrProThrIleGluAspPheHISArgIysValTyr 60
Db 136 ACCGGCGGCTTCGAGAGCGCTACACGCTTACCATTCAGAGACTTCCACCGCAAGTTCTAC 195
QY 61 AsnIleArgGlyAspMetTyrGlnLeuAspIleLeuAspThrSerGlyAsnHISProPhe 80
Db 196 TCCATCCGCGGCGAGCTTACACAGCTCGACATCTCTCGACAGTCGCGCAACCAACCGCTTC 255
QY 81 ProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeu 100
Db 256 CCGCCCATGGCGGCGCTCTCCATCTCAACAGAGACGTTTCATCTCGGTGTTCAGTCTG 315
QY 101 AspAsnArgIysSerPheAspGluValIysArgLeuGlnIysGlnIleLeuGluValIys 120
Db 316 GACAAACCGCACTCTTCAGAGAGTGTGAGGCGCTCAGGCAAGATCTTCGACACCAAG 375
QY 121 SerCysLeuIysAsnIlysrThrIysGluAlaIleGluLeuProMetValIleCysGlyAsn 140
Db 376 TCTTGCTCAAGAACAAACCAAGAGAACGTGACGTCGCCCTGTGTCATCTGCGGCAAC 435
QY 141 LysAsnAspHisGlyGluLeuCysArgGlnValProThrThrGluIleGluLeuVal 160
Db 436 AAGGGTGAACGC--GACTTCTACCGGAGGTGAGACCAAGCGCATGAGCTGTGTG 492
QY 161 SerGlyAsp--GluAsnSerAlaTyrPheGluValSerAlaIysLysAsnThrAsnVal 179
Db 493 GGGAGAGACCCCGAGCGCTGCGCTACTTCAGATCTCGGCCAAGAAAGACAGACGCTG 552
QY 180 AspGluMetPheTyrValLeuPheSerMetAlaIysLeuProHisGluMetSerProAla 199
Db 553 GACCAGATGTTCGCGCGCTCTTCGACATGCGCAAGCTGCCCAAGGATGAGCCAGAC 612
QY 200 LeuHisArgLysIleSerValGlnTyrGlyAspAlaPheHisProArgProPheCysMet 219
Db 613 CTGCAACCGCAAGGTCTGTGAGTACTGCAAGTGTGCTGCACAAAGAG--GCGCTG 666
QY 220 ArgArgValIysGluMet-----AspAla 227
Db 667 CGGAACAAGAGCTGCTGCGGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 726
QY 228 TyrGlyMetValSerProPheAlaArgArgProSerValAsnSerAspLeuIlysrTyrIle 247
Db 228 TTTGGCATGTGGACACCTTTCGCGCGCGGCCCAAGCTACACAGCACTCATGTATCATC 786
QY 248 LysAlaIysValLeuArgGluGlnAlaArgGluArgAspLysCysThrIle 265
Db 787 CGCGAAGAGCGCAGCGCGCGGCAAGCAAGAGAGCGGTGCGGTATC 840
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Search completed: April 24, 2005, 07:51:00
Job time : 680 secs